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Subject: case #09/779,323

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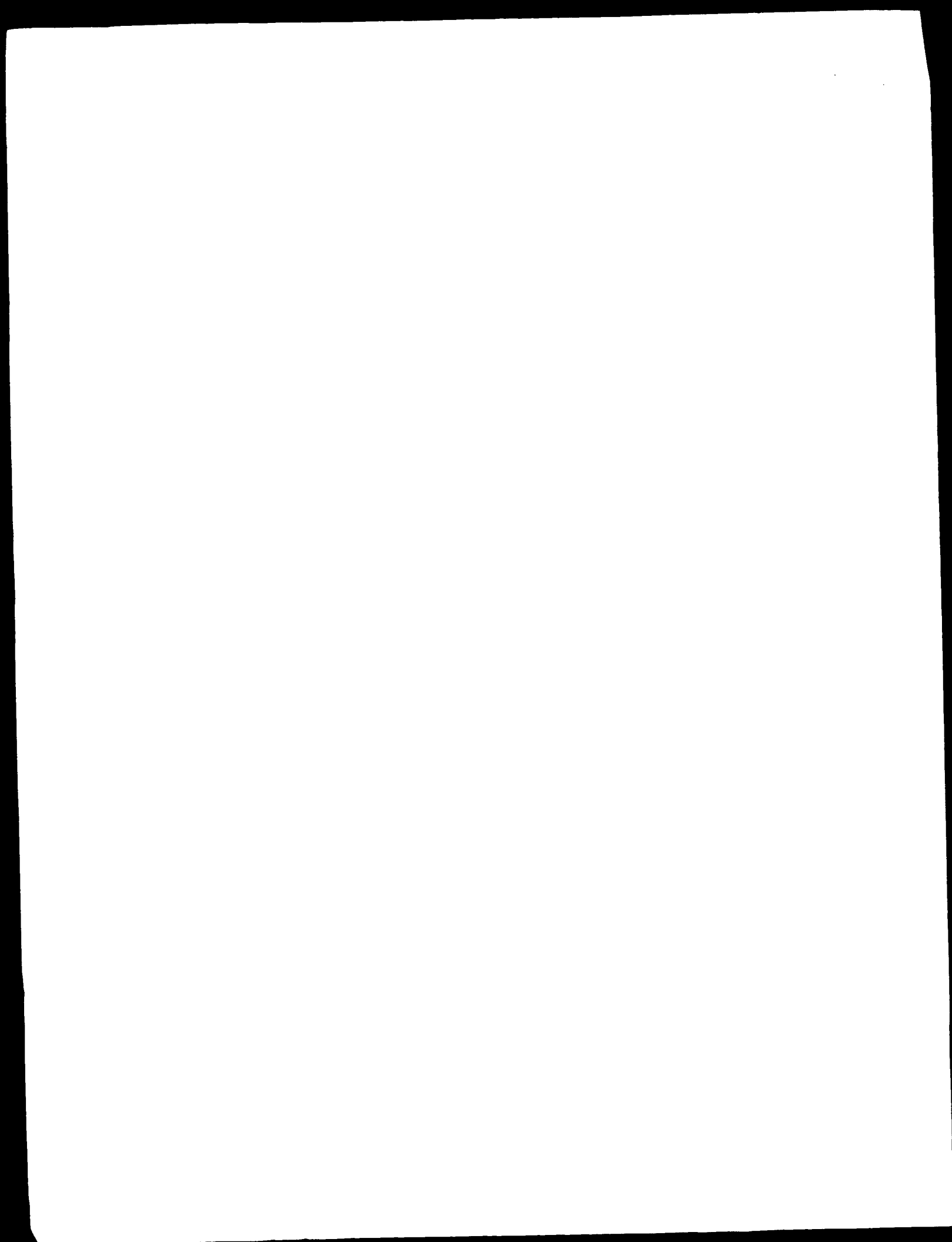
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Primary Examiner
Art Unit 1652
Mail box No. 10D01

Mary Jane Ruhl
Tech. Info. Specialist, STIC
TC-1600
DM-1, Room 6A-06
Phone: 605-1155

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Searcher Prep/Review: _____
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PS Claim 14; Page 21 22; 27pp; English.
 XX This sequence represents a novel proteolytic protein isolated from
 CC Recardiopsis sp. strain NRRL 18262. This protein may be used in
 CC for oral additives or compositions or wash liquors comprising specific
 CC branching systems.
 XX
 SQ Sequence 188 AA;
 Query Match 100.0%; Score 1005; ID 22; Length 188;
 Best Local Similarity 100.0%; Prod. No. 7.6e-76;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADTGGGLAYTMSGRGSGVFAAATNAAGQPGVTAAGHCGRVGTQVITGNRGVFFQSVFPCN 60
 DB 1 ADTGGGLAYTMSGRGSGVFAAATNAAGQPGVTAAGHCGRVGTQVITGNRGVFFQSVFPCN 60
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 DB 121 VSYFEGIVNMRTTTCAPGDSGSGSYISGTGAGCVISGSGSNCRKGTTFYQVFTHMVN 180
 QY 181 SWGVRLK 188
 DB 181 SWGVRLK 188
 RESULT 4
 ID AAM44141 standard; Protein: 475 AA.
 XX
 AC AAM44141;
 DT 05-MAY-1998 (first entry)
 XX
 DE Thermostable alkaline protease.
 XX
 KW Thermostable alkaline protease; detergent additive; fruit juice;
 KW food additive; nutraceutical; pharmaceutical.
 XX
 OS Thermomonospora fusa.
 XX
 FH Location/Qualifiers
 FT Peptide 1-181
 FT Protein Zlotekl, Sjmal
 FT 182..475
 FT Label Thermostable alkaline protease
 FT Misc-difference 143
 FT Note *Gln encoded by GAT*
 XX
 FN DS5705379-A.
 XX
 PP 06 JAN 1998.
 XX
 PP 23-OCT-1996; 960S-0736361
 XX
 PP 23-OCT-1996; 960S-0736361
 XX
 PP (CUBR) CUBRILL PES POUND INC.
 XX
 PP Lao G. Wilson DB;
 XX
 PP WPI: 1998 086147/08.
 XX
 PP N FSDR; AAV12149.
 XX
 PP DNA used in production of recombinant alkaline protease - encodind
 PP recombinant thermostable alkaline protease of Thermomonospora fusa
 XX
 PP Claim 4; Column 17 20; 14pp; English.
 PS The present sequence represents a thermostable alkaline protease from
 CC Thermomonospora fusa. The DNA encoding the protein is used for
 CC producing the recombinant alkaline protease by a method comprising
 CC culturing the cells and recovering protein from the culture medium.
 CC Alkaline proteases are used as detergent additives, for clarifying
 CC fruit juices, for preparing protein hydrolysates for use as food

PS Claim 14; Page 21 22; 27pp; English.
 XX This sequence represents a novel proteolytic protein isolated from
 CC Recardiopsis sp. strain NRRL 18262. This protein may be used in
 CC for oral additives or compositions or wash liquors comprising specific
 CC branching systems.
 XX
 SQ Sequence 188 AA;
 Query Match 100.0%; Score 1005; ID 17; Length 188;
 Best Local Similarity 100.0%; Prod. No. 7.6e-76;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADTGGGLAYTMSGRGSGVFAAATNAAGQPGVTAAGHCGRVGTQVITGNRGVFFQSVFPCN 60
 DB 1 ADTGGGLAYTMSGRGSGVFAAATNAAGQPGVTAAGHCGRVGTQVITGNRGVFFQSVFPCN 60
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 DB 61 DAAPVRGTSNFTLNILVSKNTGATTAAGHCGRVGTQVITGNRGVFFQSVFPCN 120
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 DB 121 VSYFEGIVNMRTTTCAPGDSGSGSYISGTGAGCVISGSGSNCRKGTTFYQVFTHMVN 180
 QY 181 SWGVRLK 188
 DB 181 SWGVRLK 188
 RESULT 2
 ID AAM07125 standard; Protein: 188 AA.
 XX
 AC AAM07125;
 DT 24 OCT 2001 (first entry)
 XX
 DE Nocardiopsis sp. acid-stable protease.
 XX
 KW Acid-stable protease; animal feed; nutrition; monogastric animal;
 KW human.
 XX
 OS Nocardiopsis sp. NRRL 18262.
 XX
 FN W0200158276_A2.
 XX
 PP 14 ADJ 2001.
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 PP 05 FEB 2001; 2001W01701154.
 XX
 PP 08 FEB 2000; 2000W0K-0000200.
 XX
 PP (BEEF) BOFFMANN LA RACHE & CO AG F
 XX
 PP Chesterland PK, Stockholm C;
 XX
 PP WPI: 2001-488940/54.
 XX
 PP use of acid stable protease for producing a food composition
 XX
 PP Claim 1; Page 46; 49pp; English.
 PS The invention relates to the use of at least one acid stable protease in
 CC animal feed, to improve its nutritional value and in the treatment
 CC of vegetable proteins. The feed composition is useful for feeding
 CC animals, including humans, ruminants and non ruminants i.e. monogastric
 CC animals (e.g. pigs) poultry and fish. The stomach of monogastric animals
 CC and many fish exhibit a strongly acid pH, however, most protein digestion
 CC occurs in the small intestine. Provided is a feed composition which
 CC comprises an acid stable protease that can survive passage through the
 CC stomach. The present sequence is an acid stable protease from
 CC Nocardiopsis sp. NRRL 18262.

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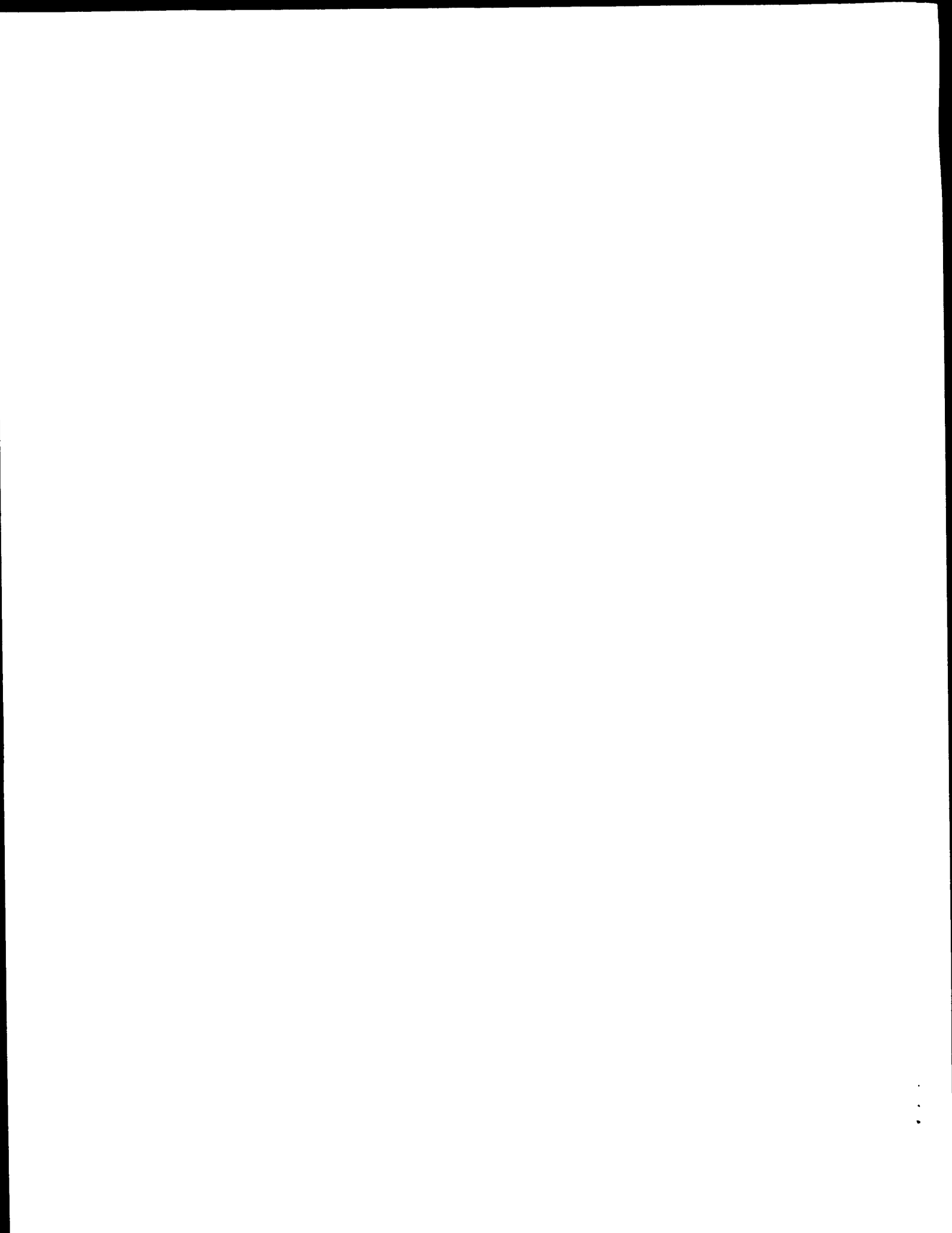
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1 Patent No. US20020127564A1
 2 GENERAL INFORMATION:
 3 APPLICANT: Baker, Kevin R.
 4 APPLICANT: Chen, Jian
 5 APPLICANT: Desnoyers, Luc
 6 APPLICANT: Goddard, Audrey
 7 APPLICANT: Gadowski, Paul J.
 8 APPLICANT: Gurney, Austin L.
 9 APPLICANT: Pan, James
 10 APPLICANT: Smith, Victor L.
 11 APPLICANT: Watanabe, Tadashi K.
 12 APPLICANT: Zhand, Zhenin
 13 TITLE OF INVENTION: SECRETED AND TRANSMUTABLE POLYMERIZATION AND NUCLEIC
 14 FILE REFERENCE: P44 40101
 15 CURRENT APPLICATION NUMBER: 60/000000
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Matches	111	Conserved	190	41	Mismatches	402	Indels	81	Gaps
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Query Match: 52.88% Score 541; 100.0% Identity 40%

Best Local Similarity: 54.28% Ident. No. 410 421

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Figure 1 illustrates the experimental setup. A subject is seated at a table, viewing a video screen. A camera is positioned above the screen. A target is located on the screen. A horizontal line is drawn on the screen, representing the target position. The subject's hand is positioned at the starting point. The distance from the starting point to the target is labeled as 'D'. The distance from the starting point to the horizontal line is labeled as 'L'. The distance from the horizontal line to the target is labeled as 'D-L'.

[illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (○), 10⁷ cells/ml (□), 10⁸ cells/ml (△), and 10⁹ cells/ml (◇). The error bars represent the standard deviation of three independent experiments.

100

Figure 1: Schematic representation of the experimental design. The diagram shows a sequence of events: 'Stimulus presentation' (a box with a question mark), 'Response' (a box with a question mark), 'Feedback' (a box with a question mark), and 'Inter-trial interval' (a box with a question mark). The sequence is repeated for multiple trials, with a 'Start' box at the beginning and an 'End' box at the end.

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[illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in the YEA medium for 24 h at 28°C. The cell concentration of the strains was adjusted to 10⁸ cells/ml. The cell suspension was then diluted with distilled water to the concentration of 10⁶ cells/ml. The cell suspension was then mixed with the plant tissue and the transformation efficiency was determined. The results are shown in Table 1.

『古今圖書集成』

[illegible]

12	118.6	11.5	2.50	21	AAV1061.1
13	111	11.0	2.50	21	AAV75.5
14	111	11.5	2.51	19	AAV75.5
15	108.5	10.8	2.50	18	AAV271.8
16	110	10.7	2.68	18	AAV271.8
17	107.5	10.7	2.53	23	AAV176.7
18	107.5	10.7	2.24	21	AAV176.7
19	107.5	10.7	2.24	1	AAV58.5
20	107.5	10.7	2.29	21	AAV774.4
21	107.5	10.7	2.81	21	AAV119.4
22	107.5	10.7	2.81	22	AAV109.6
23	107	10.6	2.80	19	AAV5.3
24	107	10.6	3.00	21	AAV224.4
25	107	10.6	3.00	21	AAV334.4
26	106	10.5	2.85	22	AAV86.1
27	105.5	10.5	2.82	22	AAV244.2
28	105	10.4	2.66	18	AAV71.5
29	105	10.4	2.68	18	AAV71.5
30	104	10.4	2.69	19	AAV31.3
31	104	10.4	2.74	11	AAV60.4
32	104	10.3	3.09	19	AAV50.1
33	103	10.3	3.09	19	AAV50.1
34	103.5	10.3	2.47	18	AAV084.7
35	102	10.1	3.02	19	AAV50.1
36	102	10.1	3.02	21	AAV229.1
37	102	10.1	3.02	21	AAV53.4
38	101.5	10.1	2.45	21	AAV59.6
39	101.5	10.1	1.60	21	AAV234.6
40	100.5	10.0	2.11	19	AAV31.3
41	100.5	10.0	2.11	21	AAV229.0
42	100.5	10.0	2.11	21	AAV59.6
43	100.5	10.0	2.46	21	AAV76.7
44	100.5	10.0	3.40	21	AAV75.5
45	100.5	10.0	4.40	22	AAV75.5

ADMINISTRATIVE

- | | |
|----------|--|
| RESULT 1 | |
| AAW2997 | |
| TD | AAW2997 standard, Protein, 100 AA |
| XX | AC |
| XX | AAW2997; |
| XX | |
| TD | 19-MAY-1999 (first entry) |
| XX | |
| TD | Noncoding-sis sp. proteolytic protein. |
| XX | |
| KW | Proteolytic protein; de novo addition with 13.1% homology |
| XX | |
| XX | Noncoding-sis sp. |
| XX | |
| PN | 1K9600013 A. |
| XX | |
| PD | 09-JAN-1996. |
| XX | |
| XX | 09-JAN-1996; 96JRK000013 A. |
| TF | |
| XX | 09-JAN-1996; 96JRK000013 A. |
| TR | |
| XX | (New) NAY Noncoding-sis. |
| PA | |
| XX | Berchert IV, E. L. et al. Science, 1996, 271 |
| TF | |
| XX | WFL, 1996, 185656/23. |
| TR | N-PSIB; AAX22416. |
| XX | |
| XX | Novel DNA constructs encoding proteolytic enzymes, and host cells comprising the DNA, useful for prepn. of enzymes |
| TF | |
| TF | claim for para. 2, 23, 27 and 28. |
| XX | |

1. *Phragmites australis* (Cav.) Trin. ex Steud.
 2. *Scirpus americanus* L.
 3. *Spartina patens* (Muhl.) B.
 4. *Spartina patens* (Muhl.) B.
 5. *Spartina patens* (Muhl.) B.
 6. *Spartina patens* (Muhl.) B.
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 9. *Spartina patens* (Muhl.) B.
 10. *Spartina patens* (Muhl.) B.

[illegible][illegible]

XX residues was isolated from *S. laticauda* No. 4744. The procedure has an optimum pH of 6.2 and a stable pH range of 4 to 14 can be used for the assignment, investigation, and synthesis of peptide chains at a defined site.

XX Sequences 457 AA

University of Michigan

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$\mathcal{H}^1(\mathbb{R}^n) \cap \mathcal{H}^1(\mathbb{R}^n) = \mathcal{H}^1(\mathbb{R}^n)$

288 *not* in the sample, even if the two groups had different probabilities of

$$\begin{pmatrix} 1 \\ \vdots \\ 0 \end{pmatrix} \in \mathbb{R}^n \quad \text{for } n \geq 1$$
$$\begin{array}{c} \text{XX} \\ \text{XX} \\ \text{AC} \end{array} \quad \text{AAU24}^{1,6,7};$$

XX
 2017年10月10日

KW: creating composite for redundancy detection, composite for redundancy detection

XX
 Strenuamque, et iussus, et optata, et
 Nunc

$$\{1, 2, 3, 4, \dots, 2n-1, 2n\}$$

18 JUN 1994; 0115-0121 H433.

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$$\text{PA} = (\text{LkX} + \text{C}) \cdot \text{X}^{-1} \cdot \text{X}$$
$$W_{\text{eff}} = 1997 - 4t_{\text{eff}}/c^2,$$

stability in presence of area or quadrant, equal in quadrant compositions, including randomly and distinguishable dot patterns.

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of viscous variety alkaliophilus No. 3 (A's series), the process has an apparent molecular weight of 19,811 (by reduction of aerylsulfate).


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1 CLASSIFICATION: 514514
2 PRIOR APPLICATION DATA:
3 AT: RICHARD H. STEWART, JR. 09/27/2001
4 FILING DATE: 20 JUN 1996
5 CLASSIFICATION: 514514
6 AT: RICHARD H. STEWART, JR. 09/27/2001
7 NAME: STEWART, Richard H.
8 REGISTRATION NUMBER: 24,713
9 REFERENCE: 09/27/2001
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (416) 595-1155
12 TELEFAX: (416) 595-1164
13 INFORMATION FOR SEQ ID NO: 16:
14 TYPE: amino acids
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 198 amino acids
17 TYPE: amino acid
18 STRANDNESS: Single
19 TOPOLOGY: Linear
20 US 09 106 466A 16

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Query Match: 66.9%, Score 470.5, Ids 4, Length 198:
Best Local Similarity 42.5%, Prod. No. 2.2e-23
Matches 85, Cons. 19/19, 0, Mismatches 67, Indels 15, Gaps 7:
07 1 AATDGLAYDGRK--GVSGVAAATNAAGSGVGTACGICGAGTGVTTGNE RNVDFQSVF 57
10 1 AATDGLAYDGRK--GVSGVAAATNAAGSGVGTACGICGAGTGVTTGNE RNVDFQSVF 59
07 58 PGRFAAVKGRITRTITLGAARHTGATTAAGA-HRGAFAASSWVKSGSTTINWRTIGAR 117
10 58 PGRFAAVKGRITRTITLGAARHTGATTAAGA-HRGAFAASSWVKSGSTTINWRTIGAR 117
07 60 PGRFAAVKGRITRTITLGAARHTGATTAAGA-HRGAFAASSWVKSGSTTINWRTIGAR 117
10 60 PGRFAAVKGRITRTITLGAARHTGATTAAGA-HRGAFAASSWVKSGSTTINWRTIGAR 117
07 118 GQSVYEDIVTIVTIRRTVVAITRERGMT SGTAGAVTISRS - GNT---RIG 168
10 118 GQSVYEDIVTIVTIRRTVVAITRERGMT SGTAGAVTISRS - GNT---RIG 168
07 169 TTFYQVTFVNVNWSGVRLT 188
10 169 TTFYQVTFVNVNWSGVRLT 188
07 176 SSTFRLQPTLSQVGLSLV 197
10 176 SSTFRLQPTLSQVGLSLV 197

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RESULT 15
US 09 106 466 16
1 Sequence 16, Applicant for: US/09106467
2 Patent No. 615,680
3 GENERAL INFORMATION:
4 APPLICANT: LEWIS, Shouq M.
5 APPLICANT: YANG, Yal Ping
6 APPLICANT: CHENG, Fole
7 APPLICANT: GOMEN, Raymond P.
8 APPLICANT: KLEIN, Michael H.
9 TITLE OF INVENTION: ANALYSIS OF BASE PHILDS HINGZ WITH REDUCED
10 TITLE OF INVENTION: PROHASE ACTIVITY
11 NUMBER OF SEQUENCES: 24
12 RESPONDENCE ADDRESS:
13 ADDRESS: Sun & McBurney
14 STREET: 6th Floor, 430 University Avenue
15 CITY: Toronto
16 STATE: Ontario
17 COUNTRY: Canada
18 ZIP: M5G 1R7
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: floppy disk
21 COMPILER: IBM PC compatible
22 OPERATING SYSTEM: PC DOS/MS DOS
23 SOFTWARE: Patent In Release #1.0, Version #1.0
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: 09/09106467
26 FILING DATE:
27 CLASSIFICATION:
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 09/09106467

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1 FILING DATE: 20 JUN 1996
2 CLASSIFICATION:
3 AT: RICHARD H. STEWART, JR.
4 NAME: STEWART, Richard H.
5 REGISTRATION NUMBER: 24,713
6 REFERENCE: 09/27/2001
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16 TOPOLOGY: Linear
17 US 09 106 467 16

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Query Match: 66.9%, Score 470.5, Ids 4, Length 198:
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07 1 AATDGLAYDGRK--GVSGVAAATNAAGSGVGTACGICGAGTGVTTGNE RNVDFQSVF 57
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07 58 PGRFAAVKGRITRTITLGAARHTGATTAAGA-HRGAFAASSWVKSGSTTINWRTIGAR 117
10 58 PGRFAAVKGRITRTITLGAARHTGATTAAGA-HRGAFAASSWVKSGSTTINWRTIGAR 117
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10 60 PGRFAAVKGRITRTITLGAARHTGATTAAGA-HRGAFAASSWVKSGSTTINWRTIGAR 117
07 118 GQSVYEDIVTIVTIRRTVVAITRERGMT SGTAGAVTISRS - GNT---RIG 168
10 118 GQSVYEDIVTIVTIRRTVVAITRERGMT SGTAGAVTISRS - GNT---RIG 168
07 169 TTFYQVTFVNVNWSGVRLT 188
10 169 TTFYQVTFVNVNWSGVRLT 188
07 176 SSTFRLQPTLSQVGLSLV 197
10 176 SSTFRLQPTLSQVGLSLV 197

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Search completed: April 4, 2002, 10:00:56
Job Time: 305 sec

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PERSET: 11

US 09 078 643-479

Sequence: 479, Application: 05/09/98/479-479

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker, Kevin P.

APPLICANT: Best, David

APPLICANT: Bushyev, Ian

APPLICANT: Eaton, Ian

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1 APPLICANT: Ferrara, Napoleone
2 APPLICANT: Filaretto, Ellen
3 APPLICANT: Ford, Sherman
4 APPLICANT: Gao, Wei Qiang
5 APPLICANT: Gether, Hanspeter
6 APPLICANT: Gethsen, Mary E.
7 APPLICANT: Goddard, Audrey
8 APPLICANT: Godowski, Paul
9 APPLICANT: Grimaldi, J. Christopher
10 APPLICANT: Gurney, Austin L.
11 APPLICANT: Hillan, Kenneth J.
12 APPLICANT: Kikavits, Yuri J.
13 APPLICANT: Kao, Sophia S.
14 APPLICANT: Napier, Mary A.
15 APPLICANT: Park, James
16 APPLICANT: Paoli, Nicholas P.
17 APPLICANT: Roy, Margaret Ann
18 APPLICANT: Shelton, David L.
19 APPLICANT: Stewart, Timothy A.
20 APPLICANT: Thomas, Daniel
21 APPLICANT: Williams, P. Mickey
22 APPLICANT: Wood, William L.
23 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleo-
24 TITLE OF INVENTION: Acids Purified the Same
25 FILE REFERENCE: P26001316
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1 GENERAL INFORMATION:
2 APPLICANT: Ashkenazi, Avi
3 APPLICANT: Baker, Kevin E.
4 APPLICANT: Bechtold, David
5 APPLICANT: Bushyev, S. Igor
6 APPLICANT: Butov, Ivan
7 APPLICANT: Fortov, Napolion
8 APPLICANT: Filatoff, Ellen
9 APPLICANT: Ford, Sherman
10 APPLICANT: Gao, Weigang
11 APPLICANT: Gertler, Hanspeter
12 APPLICANT: Gertsen, Mary E.
13 APPLICANT: Godard, Audrey
14 APPLICANT: Godowski, Paul J.
15 APPLICANT: Grimaud, J. Christopher
16 APPLICANT: Gruey, Austin G.
17 APPLICANT: Hillan, Kenneth J.
18 APPLICANT: Kiliyev, Yevgen
19 APPLICANT: Koo, Sophia S.
20 APPLICANT: Napier, Mary A.
21 APPLICANT: Pab, James
22 APPLICANT: Pardi, Nicholas P.
23 APPLICANT: Roy, Margaret Ann
24 APPLICANT: Shetty, David L.
25 APPLICANT: Stewart, Timothy A.
26 APPLICANT: Thomas, Daniel
27 APPLICANT: Williams, J. Mickey
28 APPLICANT: Wood, Will John L.
29 TITLE OF INVENTION: Sealed and Transmitted Polypeptides and Nucleic
30 FILE REFERENCE: P260016
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Age Group	Total (%)	Male (%)	Female (%)	Unknown (%)
18-24	10	10	10	10
25-34	20	20	20	20
35-44	30	30	30	30
45-54	40	40	40	40
55-64	50	50	50	50
65-74	60	60	60	60
75+	70	70	70	70

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ACKNOWLEDGMENTS

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Figure 1 is a schematic representation of the experimental design. It shows a flowchart with five main stages: 1. Selection of 1000 subjects, 2. Random assignment to two groups (500 each), 3. Training phase (10 days), 4. Test phase (10 days), and 5. Post-test phase (10 days). The groups are labeled 'Group 1' and 'Group 2'.

[illegible]

1. \mathbb{R}^n is a vector space over \mathbb{R} .

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Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

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STUDIOS VIN

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Symbol	Meaning
\mathbb{Z}	Integers
\mathbb{N}	Natural numbers
\mathbb{R}	Real numbers
\mathbb{C}	Complex numbers
\mathbb{Q}	Rational numbers
\mathbb{P}	Prime numbers
\mathbb{F}_p	Finite field with p elements
\mathbb{F}	Finite field
\mathbb{F}^n	n -dimensional vector space over \mathbb{F}
$\mathbb{F}^n[x]$	Polynomial ring over \mathbb{F}^n
$\mathbb{F}^n[x, y]$	Polynomial ring over \mathbb{F}^n in two variables
$\mathbb{F}^n[x, y, z]$	Polynomial ring over \mathbb{F}^n in three variables
$\mathbb{F}^n[x, y, z, w]$	Polynomial ring over \mathbb{F}^n in four variables
$\mathbb{F}^n[x, y, z, w, v]$	Polynomial ring over \mathbb{F}^n in five variables
$\mathbb{F}^n[x, y, z, w, v, u]$	Polynomial ring over \mathbb{F}^n in six variables
$\mathbb{F}^n[x, y, z, w, v, u, t]$	Polynomial ring over \mathbb{F}^n in seven variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s]$	Polynomial ring over \mathbb{F}^n in eight variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r]$	Polynomial ring over \mathbb{F}^n in nine variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q]$	Polynomial ring over \mathbb{F}^n in ten variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p]$	Polynomial ring over \mathbb{F}^n in eleven variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o]$	Polynomial ring over \mathbb{F}^n in twelve variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n]$	Polynomial ring over \mathbb{F}^n in thirteen variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m]$	Polynomial ring over \mathbb{F}^n in fourteen variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l]$	Polynomial ring over \mathbb{F}^n in fifteen variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k]$	Polynomial ring over \mathbb{F}^n in sixteen variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j]$	Polynomial ring over \mathbb{F}^n in seventeen variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i]$	Polynomial ring over \mathbb{F}^n in eighteen variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h]$	Polynomial ring over \mathbb{F}^n in nineteen variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g]$	Polynomial ring over \mathbb{F}^n in twenty variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f]$	Polynomial ring over \mathbb{F}^n in twenty-one variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e]$	Polynomial ring over \mathbb{F}^n in twenty-two variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d]$	Polynomial ring over \mathbb{F}^n in twenty-three variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c]$	Polynomial ring over \mathbb{F}^n in twenty-four variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b]$	Polynomial ring over \mathbb{F}^n in twenty-five variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a]$	Polynomial ring over \mathbb{F}^n in twenty-six variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z]$	Polynomial ring over \mathbb{F}^n in twenty-seven variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y]$	Polynomial ring over \mathbb{F}^n in twenty-eight variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x]$	Polynomial ring over \mathbb{F}^n in twenty-nine variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w]$	Polynomial ring over \mathbb{F}^n in thirty variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v]$	Polynomial ring over \mathbb{F}^n in thirty-one variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u]$	Polynomial ring over \mathbb{F}^n in thirty-two variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t]$	Polynomial ring over \mathbb{F}^n in thirty-three variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t, s]$	Polynomial ring over \mathbb{F}^n in thirty-four variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t, s, r]$	Polynomial ring over \mathbb{F}^n in thirty-five variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t, s, r, q]$	Polynomial ring over \mathbb{F}^n in thirty-six variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t, s, r, q, p]$	Polynomial ring over \mathbb{F}^n in thirty-seven variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t, s, r, q, p, o]$	Polynomial ring over \mathbb{F}^n in thirty-eight variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t, s, r, q, p, o, n]$	Polynomial ring over \mathbb{F}^n in thirty-nine variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t, s, r, q, p, o, n, m]$	Polynomial ring over \mathbb{F}^n in forty variables
$\mathbb{F}^n[x, y, z, w, v, u, t, s, r, q, p, o, n, m, l, k, j, i, h, g, f, e, d, c, b, a, z, y, x, w, v, u, t, s, r, q, p, o, n, m, l]$	Polynomial ring over \mathbb{F}^n in forty-one variables
$\mathbb{F}^n[x, y, z, w$	

\mathcal{F}_1 \mathcal{F}_2 \mathcal{F}_3 \mathcal{F}_4 \mathcal{F}_5 \mathcal{F}_6 \mathcal{F}_7 \mathcal{F}_8 \mathcal{F}_9 \mathcal{F}_{10} \mathcal{F}_{11} \mathcal{F}_{12} \mathcal{F}_{13} \mathcal{F}_{14} \mathcal{F}_{15} \mathcal{F}_{16} \mathcal{F}_{17} \mathcal{F}_{18} \mathcal{F}_{19} \mathcal{F}_{20} \mathcal{F}_{21} \mathcal{F}_{22} \mathcal{F}_{23} \mathcal{F}_{24} \mathcal{F}_{25} \mathcal{F}_{26} \mathcal{F}_{27} \mathcal{F}_{28} \mathcal{F}_{29} \mathcal{F}_{30} \mathcal{F}_{31} \mathcal{F}_{32} \mathcal{F}_{33} \mathcal{F}_{34} \mathcal{F}_{35} \mathcal{F}_{36} \mathcal{F}_{37} \mathcal{F}_{38} \mathcal{F}_{39} \mathcal{F}_{40} \mathcal{F}_{41} \mathcal{F}_{42} \mathcal{F}_{43} \mathcal{F}_{44} \mathcal{F}_{45} \mathcal{F}_{46} \mathcal{F}_{47} \mathcal{F}_{48} \mathcal{F}_{49} \mathcal{F}_{50} \mathcal{F}_{51} \mathcal{F}_{52} \mathcal{F}_{53} \mathcal{F}_{54} \mathcal{F}_{55} \mathcal{F}_{56} \mathcal{F}_{57} \mathcal{F}_{58} \mathcal{F}_{59} \mathcal{F}_{60} \mathcal{F}_{61} \mathcal{F}_{62} \mathcal{F}_{63} \mathcal{F}_{64} \mathcal{F}_{65} \mathcal{F}_{66} \mathcal{F}_{67} \mathcal{F}_{68} \mathcal{F}_{69} \mathcal{F}_{70} \mathcal{F}_{71} \mathcal{F}_{72} \mathcal{F}_{73} \mathcal{F}_{74} \mathcal{F}_{75} \mathcal{F}_{76} \mathcal{F}_{77} \mathcal{F}_{78} \mathcal{F}_{79} \mathcal{F}_{80} \mathcal{F}_{81} \mathcal{F}_{82} \mathcal{F}_{83} \mathcal{F}_{84} \mathcal{F}_{85} \mathcal{F}_{86} \mathcal{F}_{87} \mathcal{F}_{88} \mathcal{F}_{89} \mathcal{F}_{90} \mathcal{F}_{91} \mathcal{F}_{92} \mathcal{F}_{93} \mathcal{F}_{94} \mathcal{F}_{95} \mathcal{F}_{96} \mathcal{F}_{97} \mathcal{F}_{98} \mathcal{F}_{99} \mathcal{F}_{100}

1. *Chlorophyll a* (Chl *a*)

[illegible]

20	114	11.4	284	5	actin	actin
21	114	11.4	284	5	actin	actin
22	114	11.4	284	5	actin	actin
23	114	11.4	284	5	actin	actin
24	114	11.4	284	5	actin	actin
25	114	11.4	284	5	actin	actin
26	109.5	10.9	260	34	actin	actin
27	109.5	10.9	260	34	actin	actin
28	109	10.9	244	5	actin	actin
29	109	10.9	244	5	actin	actin
30	108.5	10.8	238	5	actin	actin
31	108.5	10.8	238	5	actin	actin
32	108	10.8	238	5	actin	actin
33	108	10.8	238	5	actin	actin
34	107.5	10.7	238	5	actin	actin
35	107.5	10.7	238	5	actin	actin
36	107	10.7	238	5	actin	actin
37	107	10.7	238	5	actin	actin
38	107	10.7	238	5	actin	actin
39	106.5	10.6	238	5	actin	actin
40	106.5	10.6	238	5	actin	actin
41	106	10.6	238	5	actin	actin
42	105.5	10.5	238	5	actin	actin
43	105.5	10.5	238	5	actin	actin
44	105.5	10.5	238	5	actin	actin
45	105	10.5	238	5	actin	actin

20	114	11.4	284	5	actin	actin
21	114	11.4	284	5	actin	actin
22	114	11.4	284	5	actin	actin
23	114	11.4	284	5	actin	actin
24	114	11.4	284	5	actin	actin
25	114	11.4	284	5	actin	actin
26	109.5	10.9	260	34	actin	actin
27	109.5	10.9	260	34	actin	actin
28	109	10.9	244	5	actin	actin
29	109	10.9	244	5	actin	actin
30	108.5	10.8	238	5	actin	actin
31	108.5	10.8	238	5	actin	actin
32	108	10.8	238	5	actin	actin
33	108	10.8	238	5	actin	actin
34	107.5	10.7	238	5	actin	actin
35	107.5	10.7	238	5	actin	actin
36	107	10.7	238	5	actin	actin
37	107	10.7	238	5	actin	actin
38	107	10.7	238	5	actin	actin
39	106.5	10.6	238	5	actin	actin
40	106.5	10.6	238	5	actin	actin
41	106	10.6	238	5	actin	actin
42	105.5	10.5	238	5	actin	actin
43	105.5	10.5	238	5	actin	actin
44	105.5	10.5	238	5	actin	actin
45	105	10.5	238	5	actin	actin

20	114	11.4	284	5	actin	actin
21	114	11.4	284	5	actin	actin
22	114	11.4	284	5	actin	actin
23	114	11.4	284	5	actin	actin
24	114	11.4	284	5	actin	actin
25	114	11.4	284	5	actin	actin
26	109.5	10.9	260	34	actin	actin
27	109.5	10.9	260	34	actin	actin
28	109	10.9	244	5	actin	actin
29	109	10.9	244	5	actin	actin
30	108.5	10.8	238	5	actin	actin
31	108.5	10.8	238	5	actin	actin
32	108	10.8	238	5	actin	actin
33	108	10.8	238	5	actin	actin
34	107.5	10.7	238	5	actin	actin
35	107.5	10.7	238	5	actin	actin
36	107	10.7	238	5	actin	actin
37	107	10.7	238	5	actin	actin
38	107	10.7	238	5	actin	actin
39	106.5	10.6	238	5	actin	actin
40	106.5	10.6	238	5	actin	actin
41	106	10.6	238	5	actin	actin
42	105.5	10.5	238	5	actin	actin
43	105.5	10.5	238	5	actin	actin
44	105.5	10.5	238	5	actin	actin
45	105	10.5	238	5	actin	actin

Best Local Similarity	Score	Prod. No.	Len	Indels	Matches	Length
Query Match	29.1%	29.1%	29.1%	16	29	29
Swat Local Similarity	40.2%	40.2%	40.2%	16	40	40
Matches	76	Conservative	33	Mismatches	73	Indels
4	110	110	110	110	110	110
5	110	110	110	110	110	110
6	110	110	110	110	110	110
7	110	110	110	110	110	110
8	110	110	110	110	110	110
9	110	110	110	110	110	110
10	110	110	110	110	110	110
11	110	110	110	110	110	110
12	110	110	110	110	110	110
13	110	110	110	110	110	110
14	110	110	110	110	110	110
15	110	110	110	110	110	110
16	110	110	110	110	110	110
17	110	110	110	110	110	110
18	110	110	110	110	110	110
19	110	110	110	110	110	110
20	110	110	110	110	110	110
21	110	110	110	110	110	110
22	110	110	110	110	110	110
23	110	110	110	110	110	110
24	110	110	110	110	110	110
25	110	110	110	110	110	110
26	110	110	110	110	110	110
27	110	110	110	110	110	110
28	110	110	110	110	110	110
29	110	110	110	110	110	110
30	110	110	110	110	110	110
31	110	110	110	110	110	110
32	110	110	110	110	110	110
33	110	110	110	110	110	110
34	110	110	110	110	110	110
35	110	110	110	110	110	110
36	110	110	110	110	110	110
37	110	110	110	110	110	110
38	110	110	110	110	110	110
39	110	110	110	110	110	110
40	110	110	110	110	110	110
41	110	110	110	110	110	110
42	110	110	110	110	110	110
43	110	110	110	110	110	110
44	110	110	110	110	110	110
45	110	110	110	110	110	110
46	110	110	110	110	110	110
47	110	110	110	110	110	110
48	110	110	110	110	110	110
49	110	110	110	110	110	110
50	110	110	110	110	110	110
51	110	110	110	110	110	110
52	110	110	110	110	110	110
53	110	110	110	110	110	110
54	110	110	110	110	110	110
55	110	110	110	110	110	110
56	110	110	110	110	110	110
57	110	110	110	110	110	110
58	110	110	110	110	110	110
59	110	110	110	110	110	110
60	110	110	110	110	110	110
61	110	110	110	110	110	110
62	110	110	110	110	110	110
63	110	110	110	110	110	110
64	110	110	110	110	110	110
65	110	110	110	110	110	110
66	110	110	110	110	110	110
67	110	110	110	110	110	110
68	110	110	110	110	110	110
69	110	110	110	110	110	110
70	110	110	110	110	110	110
71	110	110	110	110	110	110
72	110	110	110	110	110	110
73	110	110	110	110	110	110
74	110	110	110	110	110	110
75	110	110	110	110	110	110
76	110	110	110	110	110	110
77	110	110	110	110	110	110
78	110	110	110	110	110	110
79	110	110	110	110	110	110
80	110	110	110	110	110	110
81	110	110	110	110	110	110
82	110	110	110	110	110	110
83	110	110	110	110	110	110
84	110	110	110	110	110	110
85	110	110	110	110	110	110
86	110	110	110	110	110	110
87	110	110	110	110	110	110
88	110	110	110	110	110	110
89	110	110	110	110	110	110
90	110	110	110	110	110	110
91	110	110	110	110	110	110
92	110	110	110	110	110	110
93	110	110	110	110	110	110
94	110	110	110	110	110	110
95	110	110	110	110	110	110
96	110	110	110	110	110	110
97	110	110	110	110	110	110
98	110	110	110	110	110	110
99	110	110	110	110	110	110
100	110	110	110	110	110	110

Search completed: April 4, 2002, 14:00:46
 Job time: 34.8 sec

XX The invention relates to the use of at least one acid stable protease in
 XX animal feed, to improve its nutritional value and in the treatment
 XX of vegetable proteins. The feed composition is useful for feeding
 XX animals, including humans, ruminants and non ruminants i.e. monogastric
 XX animals (e.g. pigs) poultry and fish. The stomach of monogastric animals
 XX and many fish exhibit a strongly acid pH. However, most protein digestion
 XX occurs in the small intestine. Provided is a feed composition which
 XX comprises an acid stable protease that can survive passage through the
 XX stomach. The present sequence is the N terminal sequence from an
 XX acid stable protease from *Neuradiopsis alba*.

XX Sequence: 17 AA;

Query Match: 100.00; Score 89; DB 22; Length 17;

Best Local Similarity: 100.00; Prod. No. 7,66 00;

Matches: 17; Conserved: 17; Mismatches: 0; Indels: 0; Gaps: 0;

XX 1 AD1153LAY1M636SV 17

XX 1 AD1153LAY1M636SV 17

XX 1 AD1153LAY1M636SV 17

RESULT 2

AAW24567

XX AAW24567 standard: Proteolite 100 AA;

XX AAW24567;

XX AAW24567;

XX 19 MAY 1999 (first entry)

XX 19 MAY 1999 (first entry)

XX 19 MAY 1999 (first entry)

XX 19 MAY 1999 (first entry)

XX 19 MAY 1999 (first entry)

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RESULT 3

AAW24567

XX AAW24567 standard: Proteolite 100 AA;

XX AAW24567;

XX AAW24567;

XX 24 MAY 2001 (first entry)

XX 24 MAY 2001 (first entry)

XX 24 MAY 2001 (first entry)

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XX 24 MAY 2001 (first entry)

cc proteins, called pancreatic cancer antigens, given in AAB54408 to
 cc AAB5444, the human pancreatic cancer antigens have cytostatic,
 cc neuroprotective, hepatoprotective, immunomodulatory, relaxant, contractile,
 cc tumorencidal, cardiant and anti-inflammatory activities, and can be used
 cc in gene therapy. The polypeptides and proteins can be used for
 cc prevention, treatment, or amelioration of a medical condition or in assays
 cc for diagnosing a pathological condition or a susceptibility to one in a
 cc subject. Binding partners to the proteins and the activity of the
 cc proteins can be identified. The pancreatic cancer antigens can be used to
 cc detect, treat or prevent pancreatic disorders, especially cancer.
 cc Anticasts and antagagists to the antigens can be screened for.
 cc Pancreatic cancer and non polypeptides can be used to design nucleic
 cc acid hybridisation probes that can be used in chromosome mapping, linkage
 cc analysis, tissue identification and/or typing and a variety of forensic
 cc and diagnostic methods. The proteins can be used to generate antibodies
 cc which are used to purify, detect and target the polypeptides, including
 cc both in vivo and in vitro diagnostic and therapeutic methods. The
 cc proteins can be used to treat or prevent neural, immune system, muscular,
 cc reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
 cc proliferative disorders. AAB5442 to AAB5446 and AAB5447 is present
 cc sequences used in the exemplification of the present invention.

cc Sequence 112 AA;

cc Query Match 46.00; Score 4x; DB 21; Length 121;
 cc Best Local Similarity 53.90; Pred. No. 19;

cc Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

cc 97 2 DUT3GAYIM63R 14

cc 1111 111111

cc 99 DUT3GAYIM63R 112

cc RESULT 9

cc AAB5444

cc 10 AAB5444/99 standard; Protein: 124 AA;

cc AAB5444

cc 98 PER 2001 (first entry)

cc 99 Human OPEX 097563 polypeptide sequence; 330; DB No. 726;

cc 100 Human open reading frame OPEX; detect ion; cytosolic; hepatotrophic;
 cc cytotrophic; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;
 cc anticonvulsant; osteoplastic; and antitumor; immunosuppressant; cardiant;
 cc immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic;
 cc hypotensive; dermatotrophic; immunosuppressive; anti-inflammatory;
 cc antitumor; antitumor; antitumor; antitumor; antitumor;
 cc antitumor; antitumor; antitumor; antitumor; antitumor;
 cc neurodegenerative disorder; osteoarthritis; adult vs host disease;
 cc cardiovascular disease; diabetes mellitus; hypothyroidism; grip; AIDS;
 cc cholesterolemia; systemic lupus erythematosus; infection;
 cc severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 cc allergy; aplastic anaemia; neonatal haemorrhage; burn; wound;
 cc bone damage; cartilage damage; and inflammatory disease; coagulation;
 cc thrombosis; contractile;

cc Homo sapiens.

cc W22000547. A2.

cc 99 2001 2001.

cc 99 AAB 2000, 2000W0 000621.

cc 99 AAB 1999, 9900000000000000.

cc 99 AAB 1999, 9900000000000000.

cc 99 AAB 1999, 9900000000000000.

cc 99 AAB 1999, 9900000000000000.

cc 99 AAB 1999, 9900000000000000.

cc 99 AAB 1999, 9900000000000000.

cc 99 AAB 1999, 9900000000000000.

cc 99 AAB 1999, 9900000000000000.

cc Shimkova RA, Leach M;

cc 99 2001 2001 2001.

cc 99 AAB 2000, 2000W0 000621.

cc 99 AAB 1999, 9900000000000000.

cc 99 AAB 1999, 9900000000000000.

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1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

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11 MALE, LAWRENCE, J. W. JR.
12 1100 N. SYRACUSE STREET, SUITE 100
13 IN CHARGE BIRMINGHAM, AL 35203

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29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 184 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: Single
33 TOPODOLOGY: 11664
34 US-08-276 091 15

35 QUERY MATCH:
36 Best Local Similarity: 62.6% Seq. ID: 100.0% (2002)
37 Matches: 10; Conserved: 1; Mismatch: 4; Gaps: 1

38 QY 3 HIGHLYHOMO-ROSV 17
39 1 1 1 1 1 1 1 1 1 1
40 1 1 1 1 1 1 1 1 1 1

41

42 RESULT 7
43 US-08 483 859 15
44 September 15, Application in US/0440000
45 Patent No. 6,664,000

46 GENERAL INFORMATION:

47 APPLICANT: LOESMOS, Steven M.

48 APPLICANT: YANG, Yuchang

49 APPLICANT: CHENG, Yule

50 APPLICANT: CHEN, Raymond L.

51 APPLICANT: KLEIN, Aichele H.

52 TITLE OF INVENTION: Analogs of Bacteriophage Hind^{III} Protein with

53 TITLE OF INVENTION: Reduced Protease Activity

54 NUMBER OF SEQUENCES: 2

55 CORRESPONDENT ADDRESS:

56 ADDRESSEE: SEE & REFERENCE

57 STREET: Suite 700, 400 University Avenue

58 CITY: Toronto

59 STATE: Ontario

60 COUNTRY: Canada

61 ZIP: M5G 1H7

62 REGISTER FEASIBLE FORM:

63 MEDIUM TYPE: Floppy disk

64 COMPUTER: IBM PC compatible

65 OPERATING SYSTEM: PC DOS/MS-DOS

66 SOFTWARE: Patent Software #100, Version #1.2.1

67 CURRENT APPLICATION DATA:

68 APPLICATION NUMBER: 03/004,000

69 FILING DATE: 07 JUN 1995

70 CLASSIFICATION: 345

71 PRIOR APPLICATION DATA:

72 APPLICATION NUMBER: 03/004,000

73 FILING DATE: 26 JUN 1994

74 PRIOR APPLICATION DATA:

75 APPLICATION NUMBER: 03/004,000

76 FILING DATE: 21 JUL 1994

77 ATTORNEY/AGENT INFORMATION:

78 NAME: Stewart, Michael L.

79 REGISTRATION NUMBER: 24,973

80 REFERENCE/KEY NUMBER: 1000 400 000000

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82 TELEPHONE: (416) 595 1166

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84 INFORMATION FOR SEQ ID NO: 15:

85 SEQUENCE CHARACTERISTICS:

86 LENGTH: 184 amino acids

87 TYPE: amino acid

88 STRANDEDNESS: Single

89 TOPODOLOGY: 11664

90 US-08 483 859 15

91 Query Match:

92 Best Local Similarity: 62.6% Seq. ID: 100.0% (2002)

93 Matches: 10; Conserved: 1; Mismatch: 4; Gaps: 1

94 QY 3 HIGHLYHOMO-ROSV 17

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DB 1 1100LAVIM00-ROSV 17

US 08 296 149 15

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US 08 296 149 15

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Matches: 6; Conserved: 2; Mismatches: 4; Gaps: 0;
QV 4 100%
DB 52 100%
RESULTS
US 10-007-805-507
Sequence 507, Application US/10007805
Patent No. US2002/15061A1
GENERAL INFORMATION:
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APPLICANT: McNeill, Patricia D.
APPLICANT: Durham, Margaret
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND CLAIMS OF PRIORITY
FILE REFERENCE: 2002/147810
CURRENT APPLICATION NUMBER: 10/007,805
NUMBER OF SEQ. ID NOS: 54
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ. ID NO 507
LENGTH: 243
TYPE: PAT
ORGANISM: Homo sapiens
US 10-007-805-507
Query Match: 4099; Score: 41; E-Value: 1.4e-10
Best Local Similarity: 100%; E-Value: 1.4e-10
Matches: 6; Conserved: 2; Mismatches: 4; Gaps: 0;
QV 4 100%
DB 52 100%
RESULTS
US 10-007-805-507
Sequence 1547, Application US/1001547
Patent No. US2002/015061A1
GENERAL INFORMATION:
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APPLICANT: Gatti, Brian J.
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APPLICANT: Xu, H. Howard
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TITLE OF INVENTION: PROKARYOTES
FILE REFERENCE: EUTRACOLLA
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DB 52 100%
RESULTS
US 10-007-805-507
Sequence 507, Application US/10007805
Patent No. US2002/15061A1
GENERAL INFORMATION:
APPLICANT: Jillean, Yvonne
APPLICANT: Dillion, David C.
APPLICANT: Mitchell, Jennifer L.
APPLICANT: Xu, Jianchun
APPLICANT: Bartolucci, Susan L.
APPLICANT: Repler, William L.
APPLICANT: Bradshaw, Robert A.
APPLICANT: Emdin, Gary R.
APPLICANT: Veselick, Thomas S.
APPLICANT: McNeill, Patricia D.
APPLICANT: Durham, Margaret
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND CLAIMS OF PRIORITY
FILE REFERENCE: 2002/147810
CURRENT APPLICATION NUMBER: 10/007,805
NUMBER OF SEQ. ID NOS: 54
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
SEQ. ID NO 507
LENGTH: 243
TYPE: PAT
ORGANISM: Homo sapiens
US 10-007-805-507
Query Match: 4099; Score: 41; E-Value: 1.4e-10
Best Local Similarity: 100%; E-Value: 1.4e-10
Matches: 6; Conserved: 2; Mismatches: 4; Gaps: 0;
QV 4 100%
DB 52 100%
RESULTS
US 10-007-805-507
Sequence 1547, Application US/1001547
Patent No. US2002/015061A1
GENERAL INFORMATION:
APPLICANT: Basolbeck, Robert
APPLICANT: Johnson, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, John G.
APPLICANT: Veselick, Thomas S.
APPLICANT: Gatti, Brian J.
APPLICANT: Yamamoto, Robert L.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: PROKARYOTES
FILE REFERENCE: EUTRACOLLA
CURRENT APPLICATION NUMBER: 10/007,805
CURRENT FILING DATE: 2001-04-21
PRIOR APPLICATION NUMBER: 60/216,176
PRIOR FILING DATE: 2000-04-21
PRIOR APPLICATION NUMBER: 60/239,848
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: 60/237,727
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/268,627
PRIOR FILING DATE: 2000-11-27

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1 PRIOR APPLICATION NUMBER: 60/257,521
2 PRIOR FILING DATE: 2000 12-22
3 PRIOR APPLICATION NUMBER: 60/255,508
4 PRIOR FILING DATE: 2001 02-16
5 NUMBER OF SEQ ID NOS: 14110
6 SOFTWARE: FASTSEQ for Windows Version 4.0
7 SEQ ID NO: 14110
8 LENGTH: 691
9 TYPE: CDS
10 ORGANISM: Homo sapiens
11 US-09-779-323-2.rapb
12
13 Query Match: 42.7% Score: 98; ID: 10; Length: 718;
14 Best Local Similarity: 70.00; Prod. No.: 144-021
15 Matches: 7; Conservative: 1; Mismatches: 2; Gaps: 0;
16
17 4 12-LAYIMW: 13
18 47 15-LAYIMW: 66
19
20 RESULT 11
21 US-09-779-323-2.rapb
22 Sequence 14, Applied from US/09-779-323-2
23 GENERAL INFORMATION:
24 APPLICANT: Basolbeck, Robert
25 APPLICANT: Basolbeck, Robert
26 APPLICANT: Ziskind, David W.
27 APPLICANT: Wall, Daniel
28 APPLICANT: Trawick, John D.
29 APPLICANT: Carr, Grant J.
30 APPLICANT: Yamamoto, Robert J.
31 APPLICANT: Xie, H. Howard
32 TITLE OF INVENTION: Identification of Essential Genes in
33 TITLE OF INVENTION: Fishery
34 FILE REFERENCE: ELIHA-011A
35 CURRENT APPLICATION NUMBER: 60/257,521
36 PRIOR FILING DATE: 2001 03-21
37 PRIOR APPLICATION NUMBER: 60/241,078
38 PRIOR FILING DATE: 2000 09-21
39 PRIOR APPLICATION NUMBER: 60/236,842
40 PRIOR FILING DATE: 2000 05-27
41 PRIOR APPLICATION NUMBER: 60/227,227
42 PRIOR FILING DATE: 2000 05-26
43 PRIOR APPLICATION NUMBER: 60/212,573
44 PRIOR FILING DATE: 2000 10-24
45 PRIOR APPLICATION NUMBER: 60/213,625
46 PRIOR FILING DATE: 2000 11-27
47 PRIOR APPLICATION NUMBER: 60/207,931
48 PRIOR FILING DATE: 2000 12-22
49 PRIOR APPLICATION NUMBER: 60/209,408
50 PRIOR FILING DATE: 2001 02-16
51 NUMBER OF SEQ ID NOS: 14110
52 SOFTWARE: FASTSEQ for Windows Version 4.0
53 SEQ ID NO: 14110
54 LENGTH: 718
55 TYPE: CDS
56 ORGANISM: Homo sapiens
57 US-09-779-323-2.rapb

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1 PRIOR APPLICATION NUMBER: 60/257,521
2 PRIOR FILING DATE: 2000 12-22
3 PRIOR APPLICATION NUMBER: 60/255,508
4 PRIOR FILING DATE: 2001 02-16
5 NUMBER OF SEQ ID NOS: 14110
6 SOFTWARE: FASTSEQ for Windows Version 4.0
7 SEQ ID NO: 14110
8 LENGTH: 691
9 TYPE: CDS
10 ORGANISM: Homo sapiens
11 US-09-779-323-2.rapb
12
13 Query Match: 42.7% Score: 98; ID: 10; Length: 718;
14 Best Local Similarity: 70.00; Prod. No.: 144-021
15 Matches: 7; Conservative: 1; Mismatches: 2; Gaps: 0;
16
17 4 12-LAYIMW: 13
18 47 15-LAYIMW: 66
19
20 RESULT 11
21 US-09-779-323-2.rapb
22 Sequence 14, Applied from US/09-779-323-2
23 GENERAL INFORMATION:
24 APPLICANT: Basolbeck, Robert
25 APPLICANT: Basolbeck, Robert
26 APPLICANT: Ziskind, David W.
27 APPLICANT: Wall, Daniel
28 APPLICANT: Trawick, John D.
29 APPLICANT: Carr, Grant J.
30 APPLICANT: Yamamoto, Robert J.
31 APPLICANT: Xie, H. Howard
32 TITLE OF INVENTION: Identification of Essential Genes in
33 TITLE OF INVENTION: Fishery
34 FILE REFERENCE: ELIHA-011A
35 CURRENT APPLICATION NUMBER: 60/257,521
36 PRIOR FILING DATE: 2001 03-21
37 PRIOR APPLICATION NUMBER: 60/241,078
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42 PRIOR FILING DATE: 2000 05-26
43 PRIOR APPLICATION NUMBER: 60/212,573
44 PRIOR FILING DATE: 2000 10-24
45 PRIOR APPLICATION NUMBER: 60/213,625
46 PRIOR FILING DATE: 2000 11-27
47 PRIOR APPLICATION NUMBER: 60/207,931
48 PRIOR FILING DATE: 2000 12-22
49 PRIOR APPLICATION NUMBER: 60/209,408
50 PRIOR FILING DATE: 2001 02-16
51 NUMBER OF SEQ ID NOS: 14110
52 SOFTWARE: FASTSEQ for Windows Version 4.0
53 SEQ ID NO: 14110
54 LENGTH: 718
55 TYPE: CDS
56 ORGANISM: Homo sapiens
57 US-09-779-323-2.rapb

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1 PRIOR APPLICATION NUMBER: 60/257,521
2 PRIOR FILING DATE: 2000 12-22
3 PRIOR APPLICATION NUMBER: 60/255,508
4 PRIOR FILING DATE: 2001 02-16
5 NUMBER OF SEQ ID NOS: 14110
6 SOFTWARE: FASTSEQ for Windows Version 4.0
7 SEQ ID NO: 14110
8 LENGTH: 691
9 TYPE: CDS
10 ORGANISM: Homo sapiens
11 US-09-779-323-2.rapb
12
13 Query Match: 42.7% Score: 98; ID: 10; Length: 718;
14 Best Local Similarity: 70.00; Prod. No.: 144-021
15 Matches: 7; Conservative: 1; Mismatches: 2; Gaps: 0;
16
17 4 12-LAYIMW: 13
18 47 15-LAYIMW: 66
19
20 RESULT 11
21 US-09-779-323-2.rapb
22 Sequence 14, Applied from US/09-779-323-2
23 GENERAL INFORMATION:
24 APPLICANT: Basolbeck, Robert
25 APPLICANT: Basolbeck, Robert
26 APPLICANT: Ziskind, David W.
27 APPLICANT: Wall, Daniel
28 APPLICANT: Trawick, John D.
29 APPLICANT: Carr, Grant J.
30 APPLICANT: Yamamoto, Robert J.
31 APPLICANT: Xie, H. Howard
32 TITLE OF INVENTION: Identification of Essential Genes in
33 TITLE OF INVENTION: Fishery
34 FILE REFERENCE: ELIHA-011A
35 CURRENT APPLICATION NUMBER: 60/257,521
36 PRIOR FILING DATE: 2001 03-21
37 PRIOR APPLICATION NUMBER: 60/241,078
38 PRIOR FILING DATE: 2000 09-21
39 PRIOR APPLICATION NUMBER: 60/236,842
40 PRIOR FILING DATE: 2000 05-27
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43 PRIOR APPLICATION NUMBER: 60/212,573
44 PRIOR FILING DATE: 2000 10-24
45 PRIOR APPLICATION NUMBER: 60/213,625
46 PRIOR FILING DATE: 2000 11-27
47 PRIOR APPLICATION NUMBER: 60/207,931
48 PRIOR FILING DATE: 2000 12-22
49 PRIOR APPLICATION NUMBER: 60/209,408
50 PRIOR FILING DATE: 2001 02-16
51 NUMBER OF SEQ ID NOS: 14110
52 SOFTWARE: FASTSEQ for Windows Version 4.0
53 SEQ ID NO: 14110
54 LENGTH: 718
55 TYPE: CDS
56 ORGANISM: Homo sapiens
57 US-09-779-323-2.rapb

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1 PRIOR APPLICATION NUMBER: 60/257,521
2 PRIOR FILING DATE: 2000 12-22
3 PRIOR APPLICATION NUMBER: 60/255,508
4 PRIOR FILING DATE: 2001 02-16
5 NUMBER OF SEQ ID NOS: 14110
6 SOFTWARE: FASTSEQ for Windows Version 4.0
7 SEQ ID NO: 14110
8 LENGTH: 691
9 TYPE: CDS
10 ORGANISM: Homo sapiens
11 US-09-779-323-2.rapb
12
13 Query Match: 42.7% Score: 98; ID: 10; Length: 718;
14 Best Local Similarity: 70.00; Prod. No.: 144-021
15 Matches: 7; Conservative: 1; Mismatches: 2; Gaps: 0;
16
17 4 12-LAYIMW: 13
18 47 15-LAYIMW: 66
19
20 RESULT 11
21 US-09-779-323-2.rapb
22 Sequence 14, Applied from US/09-779-323-2
23 GENERAL INFORMATION:
24 APPLICANT: Basolbeck, Robert
25 APPLICANT: Basolbeck, Robert
26 APPLICANT: Ziskind, David W.
27 APPLICANT: Wall, Daniel
28 APPLICANT: Trawick, John D.
29 APPLICANT: Carr, Grant J.
30 APPLICANT: Yamamoto, Robert J.
31 APPLICANT: Xie, H. Howard
32 TITLE OF INVENTION: Identification of Essential Genes in
33 TITLE OF INVENTION: Fishery
34 FILE REFERENCE: ELIHA-011A
35 CURRENT APPLICATION NUMBER: 60/257,521
36 PRIOR FILING DATE: 2001 03-21
37 PRIOR APPLICATION NUMBER: 60/241,078
38 PRIOR FILING DATE: 2000 09-21
39 PRIOR APPLICATION NUMBER: 60/236,842
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41 PRIOR APPLICATION NUMBER: 60/227,227
42 PRIOR FILING DATE: 2000 05-26
43 PRIOR APPLICATION NUMBER: 60/212,573
44 PRIOR FILING DATE: 2000 10-24
45 PRIOR APPLICATION NUMBER: 60/213,625
46 PRIOR FILING DATE: 2000 11-27
47 PRIOR APPLICATION NUMBER: 60/207,931
48 PRIOR FILING DATE: 2000 12-22
49 PRIOR APPLICATION NUMBER: 60/209,408
50 PRIOR FILING DATE: 2001 02-16
51 NUMBER OF SEQ ID NOS: 14110
52 SOFTWARE: FASTSEQ for Windows Version 4.0
53 SEQ ID NO: 14110
54 LENGTH: 718
55 TYPE: CDS
56 ORGANISM: Homo sapiens
57 US-09-779-323-2.rapb

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ALL TRANSMISSIONS, APPLICATIONS AND NOTICES
NOT IN THE CASE

1 PRIOR APPLICATION NUMBER: 09/14844
2 PRIOR FILING DATE: 1999-09-16
3 PRIOR APPLICATION NUMBER: 09/14844
4 PRIOR FILING DATE: 1999-09-16
5 PRIOR APPLICATION NUMBER: 09/14844
6 PRIOR FILING DATE: 1999-09-16
7 PRIOR APPLICATION NUMBER: 09/14844
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96 PRIOR FILING DATE: 1999-09-16
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100 PRIOR FILING DATE: 1999-09-16

PRIOR FILING DATE: 1998 11 12
 PRIOR APPLICATION NUMBER: 09/225,442
 PRIOR FILING DATE: 2000 09 14
 PRIOR APPLICATION NUMBER: 09/488,495
 PRIOR FILING DATE: 2000 04 13
 PRIOR APPLICATION NUMBER: 09/343,465
 PRIOR FILING DATE: 2000 09 18
 PRIOR APPLICATION NUMBER: 09/665,850
 PRIOR FILING DATE: 2000 09 18
 PRIOR APPLICATION NUMBER: 09/709,248
 PRIOR FILING DATE: 2000 11 08
 PRIOR APPLICATION NUMBER: 09/667,075
 PRIOR FILING DATE: 2001 01 22
 PRIOR APPLICATION NUMBER: 09/702,794
 PRIOR FILING DATE: 2001 03 05
 PRIOR APPLICATION NUMBER: 09/688,889
 PRIOR FILING DATE: 2001 03 13
 PRIOR APPLICATION NUMBER: 09/660,288
 PRIOR FILING DATE: 2001 05 26
 PRIOR APPLICATION NUMBER: 09/695,534
 PRIOR FILING DATE: 2001 05 09
 PRIOR APPLICATION NUMBER: 09/729,605
 PRIOR FILING DATE: 2001 06 01
 PRIOR APPLICATION NUMBER: 09/665,842
 PRIOR FILING DATE: 2001 06 19
 PRIOR APPLICATION NUMBER: 09/703,717
 PRIOR FILING DATE: 1998 07 14
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 09 10
 PRIOR APPLICATION NUMBER: 09/705,067
 PRIOR FILING DATE: 1998 09 14
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 09 16
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 09 17
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 11 20
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 12 01
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 11 25
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 09 14
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 09 14
 PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 1998 09 14

Query Match: 41.6% Score: 47; 108 10; Length: 117;

Best Local Similarity: 41.6% Score: 47; 108 10;

Matches: 7; Conserved: 0; Mismatches: 4; Indels: 0; Gaps: 0;

5 GENERAL INFORMATION

34 GENERAL INFORMATION

RESULT 14
 US 09 925 400 1256
 Sequence Name: Application US/09/925,400
 Patent No.: US20010169181
 GENERAL INFORMATION
 APPLICANT: Steve Ruben
 TITLE OF INVENTION: No. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100
 FILE REFERENCE: PA101
 CURRENT APPLICATION NUMBER: 09/925,400
 PRIOR FILING DATE: 2001 08 10

PRIOR APPLICATION NUMBER: 09/703,067
 PRIOR FILING DATE: 2000 09 14
 PRIOR APPLICATION NUMBER: 09/124,270
 PRIOR FILING DATE: 1999 01 12
 NUMBER OF SEQ ID NOS: 1800
 SOFTWARE: Pat. In. Ver. 2.40
 SEQ ID NO: 1256
 LENGTH: 478
 TYPE: PFI
 ORGANISM: Homo sapiens
 FEATURE:
 ACCESSION: SITE
 LOCATION: (116)
 GENE: 100 80531; N. Xaa equals any of the characters in the list
 NAME/KEY: SITE
 LOCATOR: (104)
 OTHER INFORMATION: Xaa equals any of the characters in the list
 US 09 925 400 1256

Query Match: 41.6% Score: 47; 108 10; Length: 478;

Best Local Similarity: 41.6% Score: 47; 108 10;

Matches: 7; Conserved: 0; Mismatches: 4; Indels: 0; Gaps: 0;

5 GENERAL INFORMATION

34 GENERAL INFORMATION

RESULT 15

US 09 915 242 1002
 Sequence Name: Application US/09/915,242
 Patent No.: US20010159401
 GENERAL INFORMATION
 APPLICANT: Haselback, Robert
 APPLICANT: Carlson, Karl D.
 APPLICANT: Gaskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Lee, K. John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of human histones in

FILE REFERENCE: EXTRA-011A
 CURRENT APPLICATION NUMBER: 09/915,242
 PRIOR FILING DATE: 2001 03 21
 PRIOR APPLICATION NUMBER: 09/191,078
 PRIOR FILING DATE: 2000 04 21
 PRIOR APPLICATION NUMBER: 09/206,848
 PRIOR FILING DATE: 2000 05 24
 PRIOR APPLICATION NUMBER: 09/207,727
 PRIOR FILING DATE: 2000 05 26
 PRIOR APPLICATION NUMBER: 09/242,508
 PRIOR FILING DATE: 2000 10 24
 PRIOR APPLICATION NUMBER: 09/242,508
 PRIOR FILING DATE: 2000 11 27
 PRIOR APPLICATION NUMBER: 09/297,941
 PRIOR FILING DATE: 2000 12 22
 PRIOR APPLICATION NUMBER: 09/299,808
 PRIOR FILING DATE: 2001 02 16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: Pat. In. Ver. 2.40
 SEQ ID NO: 1802
 LENGTH: 406
 TYPE: PFI
 ORGANISM: Salmonella typhi
 FEATURE:
 ACCESSION: EXTRA-011A
 LOCATION: (116) (406)
 OTHER INFORMATION: Xaa Any Amino Acid
 US 09 915 242 1002

Query Match: 41.6% Score: 47; 108 10; Length: 406;

United Nations Security Council
Resolution 1540 (2004)

Annex

10/10/2002 10:00:00 AM

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8	51.7	26.2	27	US-09	156	4	10047	Sequence 10047, A
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11	51.7	6.24	1	US-09	764	63	10047	Sequence 10047, A
12	51.7	6.24	1	US-09	764	63	10047	Sequence 10047, A
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14	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
15	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
16	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
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23	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
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33	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
34	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
35	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
36	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
37	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
38	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
39	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
40	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
41	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
42	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
43	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
44	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A
45	51.7	6.24	21	US-09	764	63	10047	Sequence 10047, A

APPENDIX

US-09-779-323-2

Sequence 2, Appl 10047, US-09-779-323-2

GENERAL INFORMATION

APPLICANT: F. Hoffmann-La Roche AG

TITLE OF INVENTION: Use of Act1 Stat to Treat Diseases in Adult Post

PRIOR REFERENCE: 10047, 2004-000

CURRENT APPLICANT: F. Hoffmann-La Roche AG

CURRENT FILING DATE: 2004-02-08

NUMBER OF SEQ: 10-000

SOFTWARE: Patent 10-000-000

SEQ ID NO: 2

LENGTH: 17

TYPE: 100

ORGANISM: Neisseria meningitidis

US-09-779-323-2

Query Match

Best Local Similarity: 100.00

Matches: 17

US-09-779-323-2

Sequence 1, Appl 10047, US-09-779-323-2

US-09-779-323-2

Sequence 1, Appl 10047, US-09-779-323-2

```

1 GENERAL INFORMATION:
2 APPLICANT: F. Hoffmann-Laurie AG
3 TITLE OF INVENTION: Use of Anti-CD44 Antibodies in Animal Feed
4 TITLE REFERENCE: EP0412847A2
5 CURRENT APPLICATION NUMBER: 09/077932
6 FILING DATE: 2001-02-02
7 NUMBER OF SEQ. ID NOS.: 2
8 SOFTWARE: Patent In Release #1.0
9 LENGTH: 198
10 TYPE: N
11 ORGANISM: Neosartophis sp. N003.19242
12 US 09 779 323 1
13
14 Query Match: 100.00% Score 899 DB 211 Length 188
15 Best Local Similarity: 100.00% Prod. No. 120-062
16 Matches: 172 Conservative 0 Mismatches 0 Indels 0 Gaps 0
17
18 1 ALLUSLAYIMGDSV 17
19 11111111111111111111
20
21 1 ALLUSLAYIMGDSV 17
22 11111111111111111111
23
24 RESULT 3
25 US 09 779 323 1 6092
26 Sequence 1: Application US/09/077932
27 GENERAL INFORMATION:
28 APPLICANT: Biomedix, Inc.
29 APPLICANT: Sclavo, Derek
30 TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
31 TITLE REFERENCE: EP0412847A2
32 CURRENT APPLICATION NUMBER: 09/077932
33 FILING DATE: 2001-02-02
34 NUMBER OF SEQ. ID NOS.: 2
35 SOFTWARE: Patent In Release #1.0
36 SEQ. ID NO. 1: 6092
37 LENGTH: 198
38 TYPE: N
39 ORGANISM: Streptomyces sp.
40 US 09 779 323 1 6092
41
42 Query Match: 62.10% Score 663 DB 211 Length 182
43 Best Local Similarity: 70.00% Prod. No. 609
44 Matches: 122 Conservative 21 Mismatches 21 Indels 11 Gaps 11
45
46 2 ALLUSLAYIM GDSV 17
47 11111111111111111111
48 11111111111111111111
49
50 RESULT 4
51 US 09 779 323 1
52 Sequence 1: Application US/07/77932
53 GENERAL INFORMATION:
54 APPLICANT: F. Hoffmann-Laurie AG
55 TITLE OF INVENTION: Use of Proteinase and Uses Thereof
56 NUMBER OF SEQUENCES: 2
57 CURRENT APPLICATION NUMBER: 09/077932
58 ADDRESS: Hoffmann-Laurie, Brown & Buehler
59 STREET: Three Embarcadero Center
60 CITY: San Francisco
61 STATE: CA
62 COUNTRY: USA
63 ZIP: 94111
64 COMPUTER READABLE FORM:
65 MEDIUM TYPE: floppy disk
66 SOFTWARE: IBM PC compat file
67 CURRENT APPLICATION DATA:
68 SEQ. ID NO. 1: 6092
69 LENGTH: 198
70 TYPE: N
71 ORGANISM: Streptomyces sp.
72 US 09 779 323 1

```

```

1 FILING DATE: 1997-09-08
2 CLASSIFICATION: C30
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Murphy, Lisa Beth
5 REGISTRATION NUMBER: 0149
6 FILING DATE: 1997-09-08
7 TITLE OF INVENTION: INFORMATION
8 TITLE REFERENCE: EP0412847A2
9 TELEPHONE: (415) 362-5411
10 TELEFAX: (415) 362-5411
11 INFORMATION FOR SEQ. ID NO. 1:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 91 amino acids
14 TYPE: AMINO ACIDS
15 TOPOLOGY: linear
16 MOLECULE TYPE: protein
17 FRAGMENT TYPE: N terminal
18 ORIGIN: Synthetic
19 ORGANISM: Streptomyces strains
20 US 07 718 403 1
21
22 Query Match: 57.99% Score 515 DB 211 Length 182
23 Best Local Similarity: 58.88% Prod. No. 403
24 Matches: 107 Conservative 47 Mismatches 27 Indels 11 Gaps 11
25
26 2 ALLUSLAYIM GDSV 17
27 11111111111111111111
28 2 ALLUSLAYIMGDSV 18
29 11111111111111111111
30
31 RESULT 5
32 US 08 292 924 1
33 Sequence 1: Application US/08/292924
34 GENERAL INFORMATION:
35 APPLICANT: Toyo Soda, Ltd.
36 TITLE OF INVENTION: Novel Alkaline Protease and Uses Thereof
37 NUMBER OF SEQUENCES: 2
38 CURRENT APPLICATION NUMBER: 08/292924
39 ADDRESS: J. Suzanne Siebert
40 STREET: Four Embarcadero Center, Suite 1450
41 CITY: San Francisco
42 STATE: California
43 COUNTRY: USA
44 ZIP: 94111
45 COMPUTER READABLE FORM:
46 MEDIUM TYPE: floppy disk
47 SOFTWARE: IBM PC compat file
48 OPERATING SYSTEM: PC DOS/MS DOS
49 SOFTWARE: Patent In Release #1.0, Version #1.0
50 CURRENT APPLICATION DATA:
51 SEQ. ID NO. 1: 292924
52 LENGTH: 198
53 CLASSIFICATION: C30
54 PROCP APPLICATION DATA:
55 APPLICATION NUMBER: 08/292924
56 FILING DATE:
57 ATTORNEY/AGENT INFORMATION:
58 NAME: Siebert, J. Suzanne
59 REGISTRATION NUMBER: 29769
60 FILING DATE: 2000-09-04
61 TITLE OF INVENTION: INFORMATION
62 TITLE REFERENCE: EP0412847A2
63 TELEPHONE: (415) 362-5411
64 TELEFAX: (415) 362-5411
65 INFORMATION FOR SEQ. ID NO. 1:
66 SEQUENCE CHARACTERISTICS:
67 LENGTH: 91 amino acids
68 TYPE: amino acid
69 TOPOLOGY: linear
70 MOLECULE TYPE: protein
71 FRAGMENT TYPE: N terminal
72 ORIGIN: Synthetic
73 ORGANISM: Streptomyces strains
74 US 08 292 924 1

```



```

1 APPLICANT: Biocomix, Inc.
2 TITLE OF INVENTION: New L- Amino Acids, Peptides, and Antibodies
3 FILE REFERENCE: P214
4 PRIORITY FILING DATE: 2001/04/17
5 PRIOR APPLICATION DATA REMOVED: refer to PAM or file wrapper
6 NUMBER OF SEQ ID NOS: 211
7 SOFTWARE: Patent In Ver. 2.0
8 SEQ ID NO 1410
9 LENGTH: 466
10 TYPE: PPT
11 ORGANISM: Homo sapiens
12 FEATURES:
13 NAME/KEY: C11E
14 LOCATION: (29)
15 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
16 NAME/KEY: C11E
17 LOCATION: (30)
18 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
19 NAME/KEY: C11E
20 LOCATION: (31)
21 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
22 NAME/KEY: C11E
23 LOCATION: (32)
24 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
25 US 09-791 323-2

```

```

Query Match 51.7% Score 46; 106 1; Length 466;
Best Local Similarity 50.0% Prod. No. 136-024
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

97 3 110GLAYIMGR 14
10 3 110 1 1 1 1
11 3 00 VV3LAVAVGR 60

```

```

RESULT 12

```

```

1 Sequence 142, Application P21080210824

```

```

2 GENERAL INFORMATION:

```

```

3 APPLICANT: Biocomix, Inc.

```

```

4 TITLE OF INVENTION: Prostate Cancer Expression Profiles

```

```

5 FILE REFERENCE: 90 206 361

```

```

6 CURRENT APPLICATION NUMBER: 09/206210824

```

```

7 PRIORITY FILING DATE: 2002/04/09

```

```

8 PRIOR APPLICATION NUMBER: 09/201772

```

```

9 PRIOR FILING DATE: 2001/04/06

```

```

10 PRIOR APPLICATION NUMBER: 09/201773

```

```

11 NUMBER OF SEQ ID NOS: 211

```

```

12 SOFTWARE: Patent In Version 3.1

```

```

13 SEQ ID NO 142

```

```

14 LENGTH: 624

```

```

15 TYPE: PPT

```

```

16 ORGANISM: Homo sapiens

```

```

17 US 09-791 323-2

```

```

Query Match 51.7% Score 46; 106 1; Length 624;

```

```

Best Local Similarity 50.0% Prod. No. 136-024

```

```

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

97 3 110GLAYIMGR 14
10 3 110 1 1 1 1
11 3 00 VV3LAVAVGR 60

```

```

RESULT 12

```

```

1 Sequence 142, Application P21080210824

```

```

2 GENERAL INFORMATION:

```

```

3 APPLICANT: Biocomix, Inc.

```

```

4 TITLE OF INVENTION: Prostate Cancer Expression Profiles

```

```

5 FILE REFERENCE: 90 206 361

```

```

6 CURRENT APPLICATION NUMBER: 09/206210824

```

```

7 PRIORITY FILING DATE: 2002/04/09

```

```

8 PRIOR APPLICATION NUMBER: 09/201772

```

```

9 PRIOR FILING DATE: 2001/04/06

```

```

10 NUMBER OF SEQ ID NOS: 211

```

```

11 SOFTWARE: Patent In Version 3.1

```

```

1 APPLICANT: Biocomix, Inc.
2 TITLE OF INVENTION: New L- Amino Acids, Peptides, and Antibodies
3 FILE REFERENCE: P214
4 PRIORITY FILING DATE: 2001/04/17
5 PRIOR APPLICATION DATA REMOVED: refer to PAM or file wrapper
6 NUMBER OF SEQ ID NOS: 211
7 SOFTWARE: Patent In Ver. 2.0
8 SEQ ID NO 1410
9 LENGTH: 466
10 TYPE: PPT
11 ORGANISM: Homo sapiens
12 FEATURES:
13 NAME/KEY: C11E
14 LOCATION: (29)
15 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
16 NAME/KEY: C11E
17 LOCATION: (30)
18 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
19 NAME/KEY: C11E
20 LOCATION: (31)
21 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
22 NAME/KEY: C11E
23 LOCATION: (32)
24 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
25 US 09-791 323-2

```

```

Query Match 51.7% Score 46; 106 1; Length 466;

```

```

Best Local Similarity 50.0% Prod. No. 236-024

```

```

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

97 3 110GLAYIMGR 14
10 3 110 1 1 1 1
11 3 00 VV3LAVAVGR 60

```

```

RESULT 12

```

```

1 Sequence 142, Application P21080210824

```

```

2 GENERAL INFORMATION:

```

```

3 APPLICANT: Biocomix, Inc.

```

```

4 TITLE OF INVENTION: Prostate Cancer Expression Profiles

```

```

5 FILE REFERENCE: 90 206 361

```

```

6 CURRENT APPLICATION NUMBER: 09/206210824

```

```

7 PRIORITY FILING DATE: 2002/04/09

```

```

8 PRIOR APPLICATION NUMBER: 09/201772

```

```

9 PRIOR FILING DATE: 2001/04/06

```

```

10 NUMBER OF SEQ ID NOS: 211

```

```

11 SOFTWARE: Patent In Version 3.1

```

```

12 SEQ ID NO 142

```

```

13 LENGTH: 624

```

```

14 TYPE: PPT

```

```

15 ORGANISM: Mus musculus

```

```

16 US 09-791 323-2

```

```

Query Match 51.7% Score 46; 106 1; Length 624;

```

```

Best Local Similarity 50.0% Prod. No. 236-024

```

```

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

97 3 110GLAYIMGR 14
10 3 110 1 1 1 1
11 3 00 VV3LAVAVGR 60

```

```

RESULT 12

```

```

1 Sequence 142, Application P21080210824

```

```

2 GENERAL INFORMATION:

```

```

3 APPLICANT: Biocomix, Inc.

```

```

4 TITLE OF INVENTION: Prostate Cancer Expression Profiles

```

```

5 FILE REFERENCE: 90 206 361

```

```

6 CURRENT APPLICATION NUMBER: 09/206210824

```

```

7 PRIORITY FILING DATE: 2002/04/09

```

```

8 PRIOR APPLICATION NUMBER: 09/201772

```

```

9 PRIOR FILING DATE: 2001/04/06

```

```

10 NUMBER OF SEQ ID NOS: 211

```

```

11 SOFTWARE: Patent In Version 3.1

```

```

12 SEQ ID NO 142

```

```

13 LENGTH: 624

```

```

14 TYPE: PPT

```

```

15 ORGANISM: Homo sapiens

```

```

16 US 09-791 323-2

```

10/1/02

10/1/02

10/1/02

10/1/02

10/1/02

10/1/02

10/1/02

10/1/02

10/1/02

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10/1/02

10/1/02

10/1/02

10/1/02

10/1/02

10/1/02

The first part of the paper discusses the importance of understanding the cultural context of the research. It highlights the need for researchers to be sensitive to the values and beliefs of the communities they are studying. This is particularly important in the field of education, where cultural differences can significantly impact learning outcomes.

The second part of the paper focuses on the methodology used in the study. It describes the process of selecting participants, collecting data, and analyzing the results. The authors emphasize the importance of using a mixed-methods approach to capture both quantitative and qualitative data.

The third part of the paper presents the findings of the study. It shows that there are significant differences in learning outcomes between students from different cultural backgrounds. These differences are attributed to a variety of factors, including language barriers, social norms, and access to resources.

The final part of the paper discusses the implications of the findings for education. It suggests that educators should take steps to create a more inclusive learning environment for all students. This can be done by providing additional support for students who are struggling and by incorporating culturally relevant materials into the curriculum.

Query Match 45,994 Score 497 100% 100% 100% 100%
 Best Local Similarity 45,994 100% 100% 100% 100%
 Matches 5: Observed 100 4: Mismatch 0 2: InDel 0 1: Gap 0

QY 3 HIGGLAY:MG 13
 DB 262 VLSMYYAL 31 272

RESULT 10
 US-09-724-676-50947
 : Sequence 50947, Application US/0972476A
 : GENERAL INFORMATION:
 : APPLICANT: Compugen LTD
 : TITLE OF INVENTION: Variants of alteredly specific
 : FILE REFERENCE: 1291814 Comp 136
 : CURRENT APPLICATION NUMBER: US/ 972476A
 : CURRENT FILING DATE: 2000 11 28
 : NUMBER OF SEQ ID NOS: 97222
 : SOFTWARE: Patent in version 4.2
 : SEQ ID NO 50947
 : LENGTH: 506
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-724-676-50947

Query Match 45,994 Score 497 100% 100% 100% 100%
 Best Local Similarity 45,994 100% 100% 100% 100%
 Matches 5: Observed 100 4: Mismatch 0 2: InDel 0 1: Gap 0

QY 3 HIGGLAY:MG 13
 DB 262 VLSMYYAL 31 272

RESULT 11
 US-09-724-676-50946
 : Sequence 50946, Application US/ 972476A
 : GENERAL INFORMATION:
 : APPLICANT: Compugen LTD
 : TITLE OF INVENTION: Variants of alteredly specific
 : FILE REFERENCE: 1291814 Comp 136
 : CURRENT APPLICATION NUMBER: US/ 972476A
 : CURRENT FILING DATE: 2000 11 28
 : NUMBER OF SEQ ID NOS: 97222
 : SOFTWARE: Patent in version 4.2
 : SEQ ID NO 50946
 : LENGTH: 506
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-09-724-676-50946

Query Match 45,994 Score 497 100% 100% 100% 100%
 Best Local Similarity 45,994 100% 100% 100% 100%
 Matches 5: Observed 100 4: Mismatch 0 2: InDel 0 1: Gap 0

QY 3 HIGGLAY:MG 13
 DB 262 VLSMYYAL 31 272

RESULT 12
 US-09-724-676A-09946
 : Sequence 50946, Application US/0972476A
 : GENERAL INFORMATION:
 : APPLICANT: Compugen LTD
 : TITLE OF INVENTION: Variants of alteredly specific
 : FILE REFERENCE: 1291814 Comp 136
 : CURRENT APPLICATION NUMBER: US/ 972476A
 : CURRENT FILING DATE: 2000 11 28
 : NUMBER OF SEQ ID NOS: 97222
 : SOFTWARE: Patent in version 4.2

1 SEQ ID NO 50946
2 LEWTR, GAG
3 LYPG, PR1
4 GAPANISM: Homo sapiens
US 09/724-676A 50946

Query Match 43.88% Score 399 108 53 Length 5062
Best Local Similarity 45.59% Prod. No. 1.86e+02
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 113GLAYTMRG 13
ID 262 VLDGMVVA13 272
1111 1 11

RESULT 14

US 09/724-676A 50947
1 Sequence 50947, Application US/09/24676A
2 GENERAL INFORMATION:
3 APPLICANT: Compugen Ltd.

4 TITLE OF INVENTION: Variants of alternative splicing

5 FILE REFERENCE: 129181.4 Comparison

6 CURRENT APPLICATION NUMBER: US/09/24676A

7 CURRENT FILING DATE: 2000 11 28

8 NUMBER OF SEQ ID NOS: 17222

9 SOFTWARE: Patent In Version 3.2

10 SEQ ID NO 50947

11 LEWTR, GAG

12 LYPG, PR1

13 GAPANISM: Homo sapiens

US 09/724-676A 50947

Query Match 43.88% Score 399 108 53 Length 5062
Best Local Similarity 45.59% Prod. No. 1.86e+02
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 113GLAYTMRG 13
ID 262 VLDGMVVA13 272
1111 1 11

RESULT 14

US 09/724-676A 50948
1 Sequence 50948, Application US/09/24676A
2 GENERAL INFORMATION:
3 APPLICANT: Compugen Ltd.

4 TITLE OF INVENTION: Variants of alternative splicing

5 FILE REFERENCE: 129181.4 Comparison

6 CURRENT APPLICATION NUMBER: US/09/24676A

7 CURRENT FILING DATE: 2000 11 28

8 NUMBER OF SEQ ID NOS: 17222

9 SOFTWARE: Patent In Version 3.2

10 SEQ ID NO 50948

11 LEWTR, GAG

12 LYPG, PR1

13 GAPANISM: Homo sapiens

US 09/724-676A 50948

Query Match 43.88% Score 399 108 53 Length 5062
Best Local Similarity 45.58% Prod. No. 1.86e+02
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 113GLAYTMRG 13
ID 262 VLDGMVVA13 272
1111 1 11

RESULT 14

US 09/724-676 50949
1 Sequence 50949, Application US/09/24676
2 GENERAL INFORMATION:
3 APPLICANT: Compugen Ltd.

4 TITLE OF INVENTION: Variants of alternative splicing

5 FILE REFERENCE: 129181.4 Comparison
6 CURRENT APPLICATION NUMBER: US/09/24676A
7 CURRENT FILING DATE: 2000 11 28
8 NUMBER OF SEQ ID NOS: 17222
9 SOFTWARE: Patent In Version 3.2
10 SEQ ID NO 50945
11 LEWTR, GAG
12 LYPG, PR1
13 GAPANISM: Homo sapiens
US 09/724-676 50945

Query Match 43.88% Score 399 108 53 Length 5062
Best Local Similarity 45.59% Prod. No. 1.86e+02
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 113GLAYTMRG 13
ID 262 VLDGMVVA13 272
1111 1 11

RESULT 14

US 09/724-676A 50946
1 Sequence 50946, Application US/09/24676A
2 GENERAL INFORMATION:
3 APPLICANT: Compugen Ltd.

4 TITLE OF INVENTION: Variants of alternative splicing

5 FILE REFERENCE: 129181.4 Comparison

6 CURRENT APPLICATION NUMBER: US/09/24676A

7 CURRENT FILING DATE: 2000 11 28

8 NUMBER OF SEQ ID NOS: 17222

9 SOFTWARE: Patent In Version 3.2

10 SEQ ID NO 50947

11 LEWTR, GAG

12 LYPG, PR1

13 GAPANISM: Homo sapiens

US 09/724-676A 50947

Query Match 43.88% Score 399 108 53 Length 5062
Best Local Similarity 45.59% Prod. No. 1.86e+02
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 113GLAYTMRG 13
ID 262 VLDGMVVA13 272
1111 1 11

RESULT 14

US 09/724-676A 50948
1 Sequence 50948, Application US/09/24676A
2 GENERAL INFORMATION:
3 APPLICANT: Compugen Ltd.

4 TITLE OF INVENTION: Variants of alternative splicing

5 FILE REFERENCE: 129181.4 Comparison

6 CURRENT APPLICATION NUMBER: US/09/24676A

7 CURRENT FILING DATE: 2000 11 28

8 NUMBER OF SEQ ID NOS: 17222

9 SOFTWARE: Patent In Version 3.2

10 SEQ ID NO 50948

11 LEWTR, GAG

12 LYPG, PR1

13 GAPANISM: Homo sapiens

US 09/724-676A 50948

Query Match 43.88% Score 399 108 53 Length 5062
Best Local Similarity 45.58% Prod. No. 1.86e+02
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 113GLAYTMRG 13
ID 262 VLDGMVVA13 272
1111 1 11

RESULT 14

US 09/724-676 50949
1 Sequence 50949, Application US/09/24676
2 GENERAL INFORMATION:
3 APPLICANT: Compugen Ltd.

4 TITLE OF INVENTION: Variants of alternative splicing

Query Match: 52.00% Score: 47.10 Length: 142
 Best Local Similarity: 50.00% Pred. No. 14
 Matches: 6 Conservative: 4 Mismatches: 0 Gaps: 0

2 01035AYIM6SV 17
 111 11 1111
 14 260 DAV9011YIARDNV 795

RESULT 4

34672
 A:Name: Sorine protease 1 Streptomyces sp.
 A:Species: Streptomyces sp.
 A:Date: 13 Jan 1995 #sequence revision 13 Jan 1995 #text_change 19 May 2000
 A:Accession: S44672

Ref: Yoshida, Y., Kato, T., H., Y., J.B.,
 submitted to the EMBL Data Library, July 1993
 A:Reference number: S44672

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1488
 A:Cross references: GRL29018; NID0542954; P11N:AAA26813.1; P1104542656

A:Experimental source: sorine protease
 A:Keywords: sorine protease

Query Match: 57.00% Score: 51.50 Length: 142
 Best Local Similarity: 50.00% Pred. No. 14
 Matches: 6 Conservative: 4 Mismatches: 0 Gaps: 0

2 01035AYIM6SV 17
 111 11 1111
 14 260 DAV9011YIARDNV 795

RESULT 4

34672
 A:Name: Sorine protease 1 Streptomyces sp.
 A:Species: Streptomyces sp.
 A:Date: 13 Jan 1995 #sequence revision 13 Jan 1995 #text_change 19 May 2000
 A:Accession: S44672

Ref: Yoshida, Y., Kato, T., H., Y., J.B.,
 submitted to the EMBL Data Library, July 1993
 A:Reference number: S44672

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1488
 A:Cross references: GRL29018; NID0542954; P11N:AAA26813.1; P1104542656

A:Experimental source: sorine protease
 A:Keywords: sorine protease

Query Match: 56.20% Score: 50.10 Length: 142
 Best Local Similarity: 50.00% Pred. No. 14
 Matches: 6 Conservative: 4 Mismatches: 0 Gaps: 0

2 01035AYIM6SV 17
 111 11 1111
 14 260 DAV9011YIARDNV 795

RESULT 5

34672
 A:Name: Sorine protease 1 Streptomyces sp.
 A:Species: Streptomyces sp.
 A:Date: 13 Jan 1995 #sequence revision 13 Jan 1995 #text_change 19 May 2000
 A:Accession: S44672

Ref: Yoshida, Y., Kato, T., H., Y., J.B.,
 submitted to the EMBL Data Library, July 1993
 A:Reference number: S44672

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1488
 A:Cross references: GRL29018; NID0542954; P11N:AAA26813.1; P1104542656

A:Experimental source: sorine protease
 A:Keywords: sorine protease

A:Accession: J00657
 A:Molecule type: DNA
 A:Species: Streptomyces sp.
 A:Date: 13 Jan 1995 #sequence revision 13 Jan 1995 #text_change 19 May 2000
 A:Accession: J00657

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1488
 A:Cross references: GRL29018; NID0542954; P11N:AAA26813.1; P1104542656

A:Experimental source: sorine protease
 A:Keywords: sorine protease

Query Match: 52.00% Score: 47.10 Length: 142
 Best Local Similarity: 50.00% Pred. No. 14
 Matches: 6 Conservative: 4 Mismatches: 0 Gaps: 0

2 01035AYIM6SV 17
 111 11 1111
 14 260 DAV9011YIARDNV 795

RESULT 6

34672
 A:Name: Sorine protease 1 Streptomyces sp.
 A:Species: Streptomyces sp.
 A:Date: 13 Jan 1995 #sequence revision 13 Jan 1995 #text_change 19 May 2000
 A:Accession: S44672

Ref: Yoshida, Y., Kato, T., H., Y., J.B.,
 submitted to the EMBL Data Library, July 1993
 A:Reference number: S44672

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1488
 A:Cross references: GRL29018; NID0542954; P11N:AAA26813.1; P1104542656

A:Experimental source: sorine protease
 A:Keywords: sorine protease

Query Match: 59.44% Score: 43.10 Length: 142
 Best Local Similarity: 72.70% Pred. No. 8.47
 Matches: 6 Conservative: 2 Mismatches: 0 Gaps: 0

4 1035AYIM6SV 14
 111 1111
 14 260 DAV9011YIARDNV 795

RESULT 7

34672
 A:Name: Sorine protease 1 Streptomyces sp.
 A:Species: Streptomyces sp.
 A:Date: 13 Jan 1995 #sequence revision 13 Jan 1995 #text_change 19 May 2000
 A:Accession: S44672

Ref: Yoshida, Y., Kato, T., H., Y., J.B.,
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 A:Reference number: S44672

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1488
 A:Cross references: GRL29018; NID0542954; P11N:AAA26813.1; P1104542656

A:Experimental source: sorine protease
 A:Keywords: sorine protease

Query Match: 49.44% Score: 14.10 Length: 142
 Best Local Similarity: 54.94% Pred. No. 11
 Matches: 6 Conservative: 4 Mismatches: 0 Gaps: 0

4 1035AYIM6SV 14
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 14 260 DAV9011YIARDNV 795

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Query Match
Best Local Similarity 50.4% Score 497 246.54 Identical 14.0
Matches 6: Conservation 5: Mismatch 4: Indel 3: Gaps

Q7 1 AMLI-DECELYTIM-RES 17
1 1111 111111

D6 116 AAV10305AA1-DECELYTIM 151

RESULT 7

Q70XR7
ID Q70XR7
AC Q70XR7
PRELIMINARY: PE1: 21+ AA

D4 01-DEC-2001 (11EMB)rel. 19, (revised)

D4 01-DEC-2001 (11EMB)rel. 19, (last sequence update)

D4 01-MAR-2002 (11EMB)rel. 20, (last annotation update)

DE claudin 10,
DN claudin 10,
OS brachydanio rerio (zebrafish) (Zetra-fish),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Petichthys;
OC Actinopterygii; Neopterygii; Teleostei; ostariophysi; Cypriniformes;
OC Cyprinidae; Danio,
OX NCBI_taxid 7935;
RN 111
FP SEQUENCE FROM N.A.
EX MEDLINE 2447796; PubMed 11115077
RA Kallmar R.; Nakamura S.K.; Kappert J.A.; H. Ishida A.;
FI "Expression and phylogeny of claudins in vertebrates,"
RL Proc. Natl. Acad. Sci. USA, 98(13): 12112-12117,
DR EMBL: AF454277; AAC1164.1;
DR InterPro: IPR001832; claudin;
DR InterPro: IPR004051; PMF22; claudin;
DR Pfam: PF00822; PMF22; claudin 1;
DR PROSITE: PS01343; CLAUDIN; UNKN-WN 1;
SQ SEQUENCE 219 AA: 24625 MW: 14392.6114.4.000.000.4;

Query Match
Best Local Similarity 50.4% Score 497 246.54 Identical 14.0
Matches 6: Conservation 5: Mismatch 4: Indel 3: Gaps

Q7 4 UNCLAY:MDPDSV 17
1111 1111111

D6 119 TGS11YL105H7-DM 152

RESULT 8

Q70XR7
ID Q70XR7
AC Q70XR7
PRELIMINARY: PE1: 116 AA

D4 01-NOV-1999 (11EMB)rel. 12, (revised)

D4 01-NOV-1999 (11EMB)rel. 12, (last sequence update)

D4 01-MAR-2002 (11EMB)rel. 20, (last annotation update)

DE Hypothetical protein APE2225,
DN APE2225,
OS Aeropyrum pernix,
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcaceae; Aeropyrum
OX NCBI_taxid 56636;
RN 111
FP SEQUENCE FROM N.A.
EX STRAIN K1;
PX MEDLINE 9610000; PubMed 1000000
RA Kowarabayashi Y.; Hiro Y.; Horiuchi H.; Yamazaki Y.;
RA Hiroto K.; Takahashi M.; Sekine H.; Ito T.; Akita A.; Kashi H.;
RA Hioyama A.; Fukui Y.; Naito Y.; Nishida K.; Nakamura K.;
RA Takamiya M.; Masuda S.; Funakoshi T.; Tanaka T.; Kudo Y.;
RA Yamazaki J.; Kishida N.; Inagaki A.; Aoki K.; Kato K.;
RA Nakamura Y.; Namura N.; Sako Y.; Kikuchi H.;
RT "Complete genome sequence of an aerobic hyperthermophilic
RT crenarchaeon, Aeropyrum pernix K1,"
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000063; BAA1247.1;
KW Hypothetical protein; complete genome

Query Match
Best Local Similarity 50.4% Score 497 246.54 Identical 14.0
Matches 6: Conservation 5: Mismatch 4: Indel 3: Gaps

Q7 4 UNCLAY:MDPDSV 17
1111 1111111

D6 119 TGS11YL105H7-DM 152

RESULT 8

Q70XR7
ID Q70XR7
AC Q70XR7
PRELIMINARY: PE1: 116 AA

D4 01-NOV-1999 (11EMB)rel. 12, (revised)

D4 01-NOV-1999 (11EMB)rel. 12, (last sequence update)

D4 01-MAR-2002 (11EMB)rel. 20, (last annotation update)

DE Hypothetical protein APE2225,
DN APE2225,
OS Aeropyrum pernix,
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcaceae; Aeropyrum
OX NCBI_taxid 56636;
RN 111
FP SEQUENCE FROM N.A.
EX STRAIN K1;
PX MEDLINE 9610000; PubMed 1000000
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RA Hiroto K.; Takahashi M.; Sekine H.; Ito T.; Akita A.; Kashi H.;
RA Hioyama A.; Fukui Y.; Naito Y.; Nishida K.; Nakamura K.;
RA Takamiya M.; Masuda S.; Funakoshi T.; Tanaka T.; Kudo Y.;
RA Yamazaki J.; Kishida N.; Inagaki A.; Aoki K.; Kato K.;
RA Nakamura Y.; Namura N.; Sako Y.; Kikuchi H.;
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RT crenarchaeon, Aeropyrum pernix K1,"
RL DNA Res. 6:83-101(1999).
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KW Hypothetical protein; complete genome

Query Match
Best Local Similarity 50.4% Score 497 246.54 Identical 14.0
Matches 6: Conservation 5: Mismatch 4: Indel 3: Gaps

Q7 4 UNCLAY:MDPDSV 17
1111 1111111

D6 119 TGS11YL105H7-DM 152

RESULT 8

Q70XR7
ID Q70XR7
AC Q70XR7
PRELIMINARY: PE1: 116 AA

D4 01-NOV-1999 (11EMB)rel. 12, (revised)

D4 01-NOV-1999 (11EMB)rel. 12, (last sequence update)

D4 01-MAR-2002 (11EMB)rel. 20, (last annotation update)

DE Hypothetical protein APE2225,
DN APE2225,
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OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
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PX MEDLINE 9610000; PubMed 1000000
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RA Hiroto K.; Takahashi M.; Sekine H.; Ito T.; Akita A.; Kashi H.;
RA Hioyama A.; Fukui Y.; Naito Y.; Nishida K.; Nakamura K.;
RA Takamiya M.; Masuda S.; Funakoshi T.; Tanaka T.; Kudo Y.;
RA Yamazaki J.; Kishida N.; Inagaki A.; Aoki K.; Kato K.;
RA Nakamura Y.; Namura N.; Sako Y.; Kikuchi H.;
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RT crenarchaeon, Aeropyrum pernix K1,"
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KW Hypothetical protein; complete genome

Query Match
Best Local Similarity 50.4% Score 497 246.54 Identical 14.0
Matches 6: Conservation 5: Mismatch 4: Indel 3: Gaps

Q7 4 UNCLAY:MDPDSV 17
1111 1111111

D6 119 TGS11YL105H7-DM 152

RESULT 8

Q70XR7
ID Q70XR7
AC Q70XR7
PRELIMINARY: PE1: 116 AA

D4 01-NOV-1999 (11EMB)rel. 12, (revised)

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D4 01-MAR-2002 (11EMB)rel. 20, (last annotation update)

DE Hypothetical protein APE2225,
DN APE2225,
OS Aeropyrum pernix,
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcaceae; Aeropyrum
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PX MEDLINE 9610000; PubMed 1000000
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RA Hioyama A.; Fukui Y.; Naito Y.; Nishida K.; Nakamura K.;
RA Takamiya M.; Masuda S.; Funakoshi T.; Tanaka T.; Kudo Y.;
RA Yamazaki J.; Kishida N.; Inagaki A.; Aoki K.; Kato K.;
RA Nakamura Y.; Namura N.; Sako Y.; Kikuchi H.;
RT "Complete genome sequence of an aerobic hyperthermophilic
RT crenarchaeon, Aeropyrum pernix K1,"
RL DNA Res. 6:83-101(1999).
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Query Match
Best Local Similarity 50.4% Score 497 246.54 Identical 14.0
Matches 6: Conservation 5: Mismatch 4: Indel 3: Gaps

Q7 4 UNCLAY:MDPDSV 17
1111 1111111

D6 119 TGS11YL105H7-DM 152

RESULT 8

Q70XR7
ID Q70XR7
AC Q70XR7
PRELIMINARY: PE1: 116 AA

D4 01-NOV-1999 (11EMB)rel. 12, (revised)

D4 01-NOV-1999 (11EMB)rel. 12, (last sequence update)

D4 01-MAR-2002 (11EMB)rel. 20, (last annotation update)

DE Hypothetical protein APE2225,
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OS Aeropyrum pernix,
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcaceae; Aeropyrum
OX NCBI_taxid 56636;
RN 111
FP SEQUENCE FROM N.A.
EX STRAIN K1;
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RA Kowarabayashi Y.; Hiro Y.; Horiuchi H.; Yamazaki Y.;
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RA Takamiya M.; Masuda S.; Funakoshi T.; Tanaka T.; Kudo Y.;
RA Yamazaki J.; Kishida N.; Inagaki A.; Aoki K.; Kato K.;
RA Nakamura Y.; Namura N.; Sako Y.; Kikuchi H.;
RT "Complete genome sequence of an aerobic hyperthermophilic
RT crenarchaeon, Aeropyrum pernix K1,"
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000063; BAA1247.1;
KW Hypothetical protein; complete genome

cc animal feed, to improve its nutritional value and in the treatment
cc of vegetable proteins. The feed composition is useful for feeding
cc animals, including humans, ruminants and non ruminants i.e. monogastric
cc animals (e.g. pigs) poultry and fish. The stomach of monogastric animals
cc and many fish exhibit a strongly acid pH. However, most protein digestion
cc occurs in the small intestine. Provided is a feed composition which
cc comprises an acid stable protease that can survive passage through the
cc stomach. The present sequence is the N-terminal sequence from an
cc acid stable protease from *Nocardopsis alba*.

XX Sequence 17 AA;

Query Match 100.0%; Score 89; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2; 53;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A01163LAYTMGRCSV 17
IIIIIIIIIIIIIIIIIIII

DB 1 adllqqlaytmgrcsv 17

RESULT 2
AAW24565
ID AAW24565 standard, Protein, 188 AA.

XX AAW24565;

DI 19 MAY 1997 (first entry)

XX Nocardopsis sp. proteolytic protein.

DE Proteolytic products, detergent additive, wash liquid, bleaching.

XX Nocardopsis sp.

AA DK9600013.4.

XX 09 JAN 1996.

XX 09 JAN 1996, 963K (genetic).

XX 09 JAN 1996; 966K (genetic).

XX (NWA) NWA: N080138 AF.

PI Borchert TV, Ehrlich SB, Borchert L, Ehrlich S;

XX WPI: 1996-19669/20.

DE N 1334; AAW24565.

PI Novel DNA constructs encoding proteolytic enzymes - also recombinant
PI vectors and host cells comprising the DNA, useful for prepn. of the
PI enzymes

PS claim 14; Page 21-22; 27pp; English.

XX This sequence represents a novel proteolytic protein isolated from
cc Nocardopsis sp. strain 196 NR9, 19262. This protein may be used in
cc detergent additives or compositions of wash liquids comprising specific
cc bleaching systems.

XX Sequence 188 AA;

Query Match 100.0%; Score 89; DB 17; Length 188;
Best Local Similarity 100.0%; Pred. No. 5.1e 07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A01163LAYTMGRCSV 17
IIIIIIIIIIIIIIIIIIII

DB 1 adllqqlaytmgrcsv 17

RESULT 3

AAU07125
ID AAW07125 standard, Protein, 138 AA.

XX AAW07125;

DI 24-OCT-2001 (first entry)

XX Nocardopsis sp. acid stable protease.

DE Acid stable protease; animal feed; nutrition; monogastric animal;
KW ruminant.

XX Nocardii-4-513 sp. NRRL 19262.

XX W0200158276 A2.

XX 16 AUG 2001.

DE 05-FEB-2001; 2001W01001154.

XX 08 FEB 2000; 2000W01000200.

XX (first) H-ITMARR LA R-2381 & 23 AG F.

XX Oosterbaard PR, Sjoelholm C;

XX WPI: 2001 192930/53.

PI Use of acid stable protease for producing a feed composition

XX claim 1, Page 48, 49pp; English.

XX The invention relates to the use of at least one acid stable protease in
cc animal feed to improve the nutritive value of feed for treatment
cc of vegetable proteins. The feed composition is useful for feeding
cc animals, including humans, ruminants and non ruminants i.e. monogastric
cc animals (e.g. pigs) poultry and fish. The stomach of monogastric animals
cc and many fish exhibit a strongly acid pH. However, most protein digestion
cc occurs in the small intestine. Provided is a feed composition which
cc comprises an acid stable protease that can survive passage through the
cc stomach. The present sequence is an acid stable protease from
cc Nocardopsis sp. NRRL 19262.

XX Sequence 188 AA;

Query Match 100.0%; Score 89; DB 22; Length 188;
Best Local Similarity 100.0%; Pred. No. 5.1e 07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A01163LAYTMGRCSV 17

IIIIIIIIIIIIIIIIIIII

DB 1 adllqqlaytmgrcsv 17

RESULT 4

AAW24565
ID AAW24565 standard, Protein, 181 AA.

XX AAW24565;

XX 05-NOV-1997 (first entry)

XX Serine protease N terminal sequence.

XX Serine protease, N terminal; Streptomyces; filamentous; free-living; protease;
KW cleaning composition; laundry detergent; addition composition; enzyme;
KW dishwasher detergent; drain opener; area, contact lens cleaner;
KW proteinaceous stain.

XX Streptomyces griseus variety ATCC 15216; No. 24.

12 JAN 2001 2:00pm (pmc)
(SHE) SCHERING NPL

Hosted by: Brian A., Wain IX

WHL: 2001 442147/1

New nucleic acid molecules encoding eveninlinin pathway de-
products, useful for improving yields of eveninlinin, and reduce new
eveninlinin and as probes to identify homologous sequences

Claim 19: Fig 11; Doppel-Bathsh

The sequence is a subunit biosynthesis of eveninlinin.
The protein comprises one of the enzymes of the eveninlinin
pathway. The protein is a subunit of the eveninlinin
M. carbonaria eveninlinin biosynthesis pathway. The protein
is useful for selection for a transfection of transgenic host cells. An
intermediate version of the vector is useful for introducing a
eveninlinin pathway gene (a bottle-neck gene) into an eveninlinin
the genus Microsporida. The DNA encoding the biosynthetic proteins is
useful for synthesizing novel eveninlinin related compounds, analysis
from modifications of the DNA sequence designed to change glycosyl and
modified on-site amino acid groups contained in eveninlinin. For
expressed functional or mutant eveninlinin biosynthetic enzyme for
evaluation, diagnosis and preferably biosynthesis of eveninlinin or
other secondary metabolic products, improving the yield of eveninlinin
and to produce novel eveninlinin and also as a hybridisation probe to
identify homologous sequences. The encoded polypeptides are useful for
combinatorial biosynthesis to generate libraries of orthologues, e.g.
eveninlinin analogues/homologues and drug discovery. The
DNA encoding the interase allows for increasing a given gene's size, the
heterologous vector can be used to permanently differentiate copies of a
intermediate gene of choice into chromosomes of different hosts and to
integrate genes which increase the yield of known products and to
novel products such as hybrid and libraries of other novel secondary
metabolites. The vector can also be used to generate antibiotic
resistance genes in order to carry out large scale screenings with compounds to
which the strain is normally sensitive and is thus used in the identification
of processes involving eveninlinin. Strains may be identified.

Sequence: 412 AA:

Query Match: 47.2% Score: 43.0 E-10.0 Length: 412
Best Local Similarity: 70.0% (1104, No. 16)
Matches: 71 Conserved: 150 23 Mismatch: 11 Gaps: 1

QY A LKRLAYDMS 12
D 33 1 111
DB 350 1994daytar 459

RESULTS: 10
AAM10700
ID AAM10700 Standard: 1 100% (100 AA)
AC AAM10700
XX AAM10700

DI 12-OCT-2001 (first entry)

XX Peptide #492 encoded by probe for measurement of eveninlinin gene expression

XX Peptide #492 encoded by probe for measurement of eveninlinin gene expression

XX Peptide #492 encoded by probe for measurement of eveninlinin gene expression

XX Peptide #492 encoded by probe for measurement of eveninlinin gene expression

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XX Peptide #492 encoded by probe for measurement of eveninlinin gene expression

XX Peptide #492 encoded by probe for measurement of eveninlinin gene expression

XX Peptide #492 encoded by probe for measurement of eveninlinin gene expression

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10 03 SEP 2000; 2000US 0243659.
XX 04 SEP 2000; 2000US 0624263.
11 (B) (2) / MIDDLESEX GRANARY INC.
XX 04 FEB 2000; 2000US 0180412.
XX 26 MAY 2000; 2000US 0207456.
XX 30 JUN 2000; 2000US 0608408.
XX 03 AUG 2000; 2000US 0632466.
XX 21 SEP 2000; 2000US 0254087.
XX 27 SEP 2000; 2000US 0246659.
XX 04 OCT 2000; 2000US 0624263.
12 (B) (2) / MIDDLESEX GRANARY INC.
XX 06 JUN 83; Hanzel BK; Chen W; Rank DR;
XX WP: 2001-48890/53.
XX Human genome-derived single exon nucleic acid probes useful for
P1 analyzing gene expression in human cervical epithelial cells.
XX Claim 27; SEQ ID No 23384; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
XX (SNPs; see AAI16068 AAI28459). The present sequence is a peptide encoded
XX by one such probe, the SNPs are derived from human beta cells. The SNPs
XX can be used to produce a single exon microarray, which can be used for
XX measuring human gene expression in a sample derived from human cervical
XX epithelial cells. By measuring gene expression, the probes are therefore
XX useful in stratifying and/or studying of diseases of the cervix, notably
XX cervical cancer.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at http://wipo.int/pat/published\_pat\_sequences.
XX Sequence 185 AA:

Query Match. 46.1%; Score 41; 19 22; Length 196;
Best Local Similarity 46.2%; Prod. No. 37;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

V) 111GATGATGAGGCT 15
111 1 1 1
D) 53 V1842211466 65

RESULT 12
AA080999
ID AA080999 Standard; Protein; 327 AA.
XX A*
XX WP: 20 JUN 2001 (first entry)
XX 20 JUN 2001 (first entry)
XX barley iron absorption improver.
XX Barley: iron absorption improver; 1d56; 2 minutes.
XX random sequence.
XX DN J0200101191 A
XX 21 JAN 2002
XX 09 JUL 1999; 99JP 0196155.
XX 09 JUL 1999; 99JP 0196155.
XX (KAKA) KAKA000100100 SHINKO JAPAN
XX WP: 2001-55437/40.
XX N 150H; AAI04427; AAI04529; AAI04539.
XX New gene encoding a 6 kDa protein is useful as an iron absorption
XX for iron deficient barley roots
XX Table 2; Page 15; 28pp; Japanese.
XX the present sequence is the protein sequence for an iron absorption
XX improver; (left) for Gramineae, the random sequence for this protein was
XX derived from iron deficient barley roots.
XX Sequence 427 AA:

Query Match. 44.9%; Score 40; 19 22; Length 196.

```

```

10 03 SEP 2000; 2000US 0243659.
XX 04 SEP 2000; 2000US 0624263.
11 (B) (2) / MIDDLESEX GRANARY INC.
XX 04 FEB 2000; 2000US 0180412.
XX 26 MAY 2000; 2000US 0207456.
XX 30 JUN 2000; 2000US 0608408.
XX 03 AUG 2000; 2000US 0632466.
XX 21 SEP 2000; 2000US 0254087.
XX 27 SEP 2000; 2000US 0246659.
XX 04 OCT 2000; 2000US 0624263.
12 (B) (2) / MIDDLESEX GRANARY INC.
XX 06 JUN 83; Hanzel BK; Chen W; Rank DR;
XX WP: 2001-48890/53.
XX Human genome-derived single exon nucleic acid probes useful for
P1 analyzing gene expression in human placenta.
XX Claim 27; SEQ ID No 42889; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SNPs;
XX see AAI17544). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX prediction, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for differential diagnosis of
XX human genetic disorders.
XX Sequence 185 AA:

Query Match. 46.1%; Score 41; 19 22; Length 196;
Best Local Similarity 46.2%; Prod. No. 37;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

V) 111GATGATGAGGCT 15
111 1 1 1
D) 53 V1842211466 65

RESULT 12
AA080999
ID AA080999 Standard; Protein; 327 AA.
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XX DN J0200101191 A
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XX Table 2; Page 15; 28pp; Japanese.
XX the present sequence is the protein sequence for an iron absorption
XX improver; (left) for Gramineae, the random sequence for this protein was
XX derived from iron deficient barley roots.
XX Sequence 427 AA:

Query Match. 44.9%; Score 40; 19 22; Length 196.

```


1 COMPILER: IBM PC COMPATIBLE
 2 OPERATING SYSTEM: OS/2 2.00 007
 3 SOFTWARE: Patent In Release #1.0, Version #1.00
 4 CURRENT APPLICATION DATA:
 5 APPLICATION NUMBER: 09/097460-15
 6 FILING DATE: 20-JUN 1996
 7 CLASSIFICATION: 514
 8 ATTORNEY/AGENT INFORMATION:
 9 NAME: Stewart, Michael L.
 10 REGISTRATION NUMBER: 24,974
 11 REFERENCE/KEY NUMBER: 100-000
 12 TELECOMMUNICATION INFORMATION:
 13 TELEPHONE: (416) 595-1155
 14 TELEFAX: (416) 595-1154
 15 INFORMATION FOR SEQ ID NO: 1:
 16 SEQUENCE CHARACTERISTICS:
 17 LENGTH: 181 amino acids
 18 TYPE: amino acid
 19 STRANDEDNESS: single
 20 TOPOLOGY: linear
 21 US 09 615 271-15

Query Match 44.4% Score 39.5% ID: 2 Length 181
 Best Local Similarity 62.5% Prod. No. 29
 Matches 10: Conservative 1: Mismatches 4: Indels 1: Gaps 1:

07 3 (1)GLAYMAG RCSV 17
 14 1 (1)GLAYMAG RCSV 16

RESULT 14
 US 09 615 271-15
 1 Sequence 15, Application US/0907460-15
 2 Patent No. 615242
 3 GENERAL INFORMATION:
 4 APPLICANT: LOOSMORE, Steven M.
 5 APPLICANT: YAGI, Yoko
 6 APPLICANT: YAGI, Yoko
 7 APPLICANT: YAGI, Yoko
 8 APPLICANT: YAGI, Yoko
 9 APPLICANT: YAGI, Yoko
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1 TELEPHONE: (416) 595-1155
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 3 INFORMATION FOR SEQ ID NO: 1:
 4 SEQUENCE CHARACTERISTICS:
 5 LENGTH: 181 amino acids
 6 TYPE: amino acid
 7 STRANDEDNESS: single
 8 TOPOLOGY: linear
 9 US 09 074 660-15
 10 Query Match 44.4% Score 39.5% ID: 2 Length 181
 11 Best Local Similarity 62.5% Prod. No. 29
 12 Matches 10: Conservative 1: Mismatches 4: Indels 1: Gaps 1:
 13 07 3 (1)GLAYMAG RCSV 17
 14 1 (1)GLAYMAG RCSV 16
 15 RESULT 14
 16 US 09 074 659-15
 17 Sequence 15, Application US/0907460-15
 18 Patent No. 615242
 19 GENERAL INFORMATION:
 20 APPLICANT: LOOSMORE, Steven M.
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1 TITLE OF INVENTION: Use of Acid Stable Proteases in Animal Feed
 2 FILE REFERENCE: 1094,204,4
 3 CURRENT APPLICATION NUMBER: 09/09,292,924
 4 PUBLICATION DATE: 2001-02-08
 5 NUMBER OF SEQ ID NOS: 2
 6 SOFTWARE: Patent In Version 4.0
 7 SEQ ID NO: 1
 8 LENGTH: 128
 9 TYPE: PRT
 10 ORGANISM: Neorhomboides sp. NRRL 18262
 11 US 09/779-323-2

Query Match: 100.00% Score: 89; DB: 21; Length: 188;
 Best Local Similarity: 100.00% Prod. No.: 3; 4;
 Matches: 10; Conserved: 4; Mismatches: 0; Gaps: 0;

97 1 A:100%AVIM:00SV 17
 100 1 A:100%AVIM:00SV 17

RESULT 3
 US 07/718-403-1
 1 Sequence: 1; Application: 09/09,292,924
 2 GENERAL INFORMATION:
 3 APPLICANT: Lehigh University
 4 TITLE OF INVENTION: Novel Protease and Uses Thereof
 5 NUMBER OF SEQUENCES: 2
 6 CURRENT APPLICATION NUMBER: 09/09,292,924
 7 ADDRESS: Molecular Biology, Biotech & Biocore
 8 STREET: Three Embarcadero Center
 9 CITY: San Francisco
 10 STATE: CA
 11 COUNTRY: USA
 12 ZIP: 94111
 13 COMPUTER RELEASABLE FORM:
 14 MEDIUM TYPE: floppy disk
 15 COMPUTER: IBM PC compatible
 16 OPERATING SYSTEM: PC DOS/MS DOS
 17 SOFTWARE: Patent In Release #1.0, Version #1.05
 18 CURRENT APPLICATION DATA:
 19 FILING DATE: 09/09/2001
 20 FILING DATE: 19910618
 21 CLASSIFICATION: 536
 22 NAME: Matthew Lisabeth, Jr.
 23 REGISTRATION NUMBER: 21447
 24 REFERENCE/ZIP/KEY NUMBER: 17052-003
 25 REGISTRATION NUMBER: 21447
 26 TELEPHONE: (415) 393-2403
 27 TELEFAX: (415) 393-2403
 28 INFORMATION FOR SEQ ID NO: 1:
 29 SEQUENCE CHARACTERISTICS:
 30 LENGTH: 81 amino acids
 31 TYPE: Lysine-rich
 32 MOLECULE TYPE: protein
 33 FRAGMENT TYPE: N-terminal
 34 ORGANISM: Streptomyces griseus

Query Match: 57.99% Score: 51.5; DB: 3; Length: 81;
 Best Local Similarity: 58.80% Prod. No.: 3; 4;
 Matches: 10; Conserved: 4; Mismatches: 0; Gaps: 1;

97 2 100%AVIM:00SV 17
 100 2 100%AVIM:00SV 17

RESULT 4
 US 08/292-924-1
 1 Sequence: 1; Application: 09/09,292,924
 2 GENERAL INFORMATION:
 3 APPLICANT: Lehigh University
 4 TITLE OF INVENTION: Novel Alkaline Protease and Uses Thereof
 5 NUMBER OF SEQUENCES: 2
 6 CURRENT APPLICATION NUMBER: 09/09,292,924
 7 ADDRESS: J. Suzanne Stodart
 8 STREET: Four Embarcadero Center, Suite 115
 9 CITY: San Francisco
 10 STATE: California
 11 COUNTRY: USA
 12 ZIP: 94111
 13 COMPUTER RELEASABLE FORM:
 14 MEDIUM TYPE: floppy disk
 15 COMPUTER: IBM PC compatible
 16 OPERATING SYSTEM: PC DOS/MS DOS
 17 SOFTWARE: Patent In Release #1.0, Version #1.05
 18 CURRENT APPLICATION DATA:
 19 FILING DATE: 09/09/2001
 20 FILING DATE: 19910618
 21 CLASSIFICATION: 435
 22 NAME: Suzanne Stodart, J. Suzanne
 23 REGISTRATION NUMBER: 287,004
 24 REFERENCE/ZIP/KEY NUMBER: 400,04-1
 25 REGISTRATION NUMBER: 287,004
 26 TELEPHONE: (415) 362-5506
 27 TELEFAX: (415) 362-5418
 28 INFORMATION FOR SEQ ID NO: 1:
 29 SEQUENCE CHARACTERISTICS:
 30 LENGTH: 81 amino acids
 31 TYPE: Lysine-rich
 32 MOLECULE TYPE: protein
 33 FRAGMENT TYPE: N-terminal
 34 ORGANISM: Streptomyces griseus

Query Match: 57.99% Score: 51.5; DB: 3; Length: 81;
 Best Local Similarity: 58.80% Prod. No.: 3; 4;
 Matches: 10; Conserved: 4; Mismatches: 0; Gaps: 1;

97 2 100%AVIM:00SV 17
 100 2 100%AVIM:00SV 17

RESULT 5
 US 08/178-307-003
 1 Sequence: 3; Application: 08/00,090,760
 2 GENERAL INFORMATION:
 3 APPLICANT: B. NAYZIL VIVIAN
 4 TITLE OF INVENTION: NOVEL HUMAN KINASE INHIBITOR, NOVEL
 5 METHOD OF IDENTIFICATION, AND POLYPEPTIDES ENCODING HUMAN KINASE INHIBITOR AND USES
 6 NUMBER OF SEQUENCES: 3
 7 FILE REFERENCE: 01000209
 8 CURRENT APPLICATION NUMBER: 08/00,090,760
 9 CURRENT FILING DATE: 2000-01-27
 10 NUMBER OF SEQ ID NOS: 4190
 11 SOFTWARE: FASTSEQ for Windows Version: 4.0
 12 SEQ ID NO: 6013
 13 LENGTH: 142
 14 TYPE: PRT
 15 ORGANISM: HUMAN
 16 FEATURE:
 17 NAME/KEY: VARIANT

US-095902	540-14954	49,496	55,646	14,246	10,646	990
Query Match		81,092	Prod. No.	6,400,000		
Best Local Similarity	91	Conservative	91	MissMatches	91	5492
Matches	4	10GLAYTM3BP	14			
		1	111	1741		
DB	760	18GLAYTM3BR	800			

1 : Sequence 636, Application 197/US-055989
2 : GENERAL INFORMATION
3 : APPLICANT: Citicor Region,
4 : APPLICAND: Steve Rubin
5 : TITLE OF INVENTION: Human Factors and Parameters of
6 : TITLE OF INVENTION: Psychoprolides
7 : FILE REFERENCE: Patent
8 : CURRENT APPLICANT NUMBER: 197/US-055989
9 : CURRENT FILING DATE: 2000-05-08
10 : EARLIER APPLICANT NUMBER: 197/124,270
11 : EARLIER FILING DATE: 1999-04-12
12 : NUMBER OF PAGES: 928

```

? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (s)
? CHG: CH-36A11; R. Xaa equals any of the naturally occurring L-amino acids
? FEATURE:
? NAME/KEY: SITE
? LOCATION: (s)
? OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
P01-0300-05989 646

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Environ	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Environ	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Environ	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Environ	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Environ	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Environ	1	2	3	4	5																																																																																															

```

1 Sequence: 630, App Filed from US/99/25,277
2
3 GENERAL INFORMATION
4
5 APPLICANT: KOSOVA, GJ.
6
7 TITLE OF INVENTION: Nucleic Acids, Proteins and Antipeptides
8
9 FILE REFERENCE: PAl05
10
11 CURRENT APPLICANT NUMBER: 02579925,277
12
13 CURRENT FILING DATE: 2001.09.10
14
15 PREVIOUS FILING DATE: 2001.03.09
16
17 PRIOR FILING DATE: 2000.03.09
18
19 PRIOR APPLICANT NUMBER: 69/124,276
20
21 PRIOR FILING DATE: 1999.03.12
22
23 HYPOTHESIS: 112, 113, 201, 926
24
25 SOFTWARE: Patent in Vol. 2, 0
26
27 SEQ ID NO 630
28
29 LENGTH: 118
30
31 TYPE: PRI
32
33 ORGANISM: H-mn, 8-41-cmps
34
35 FEATURE:
36
37 NAME/KEY: SITE

```


Job: 09-11-02

1. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

2. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

3. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

4. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

5. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

6. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

7. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

8. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

9. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

10. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

11. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

12. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

13. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

14. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

15. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

16. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

17. 0.1% (w/v) of the sample in 0.1M Tris-HCl, pH 7.4

1. The first part of the document discusses the importance of maintaining accurate records of all transactions and activities. It emphasizes that proper record-keeping is essential for transparency and accountability, particularly in financial matters. The text outlines various methods for organizing and storing data, including digital databases and physical filing systems. It also mentions the need for regular audits and reviews to ensure the integrity of the information.

2. The second part of the document focuses on the role of communication in achieving organizational goals. It highlights the importance of clear and concise communication, both internally and externally. The text provides guidelines for effective communication, such as using appropriate language, listening actively, and providing feedback. It also discusses the benefits of open communication and how it can foster a collaborative work environment.

3. The third part of the document addresses the issue of time management. It recognizes that time is a valuable resource and that efficient use of time is crucial for productivity. The text offers several strategies for managing time effectively, including prioritizing tasks, setting deadlines, and delegating responsibilities. It also mentions the importance of taking breaks and avoiding procrastination.

4. The fourth part of the document discusses the importance of continuous learning and development. It emphasizes that in a rapidly changing world, individuals and organizations must stay up-to-date with the latest knowledge and skills. The text outlines various ways to promote learning, such as providing training opportunities, encouraging self-learning, and fostering a culture of innovation. It also mentions the importance of evaluating the effectiveness of learning initiatives.

5. The fifth part of the document discusses the importance of maintaining a positive and healthy work environment. It recognizes that a supportive and motivating work environment is essential for employee well-being and productivity. The text provides guidelines for creating a positive work environment, such as promoting work-life balance, encouraging teamwork, and addressing workplace issues promptly. It also mentions the importance of regular communication and feedback.

6. The sixth part of the document discusses the importance of maintaining accurate financial records. It emphasizes that proper financial management is essential for the long-term success of any organization. The text outlines various methods for tracking and analyzing financial data, including budgeting, accounting, and financial reporting. It also mentions the importance of maintaining accurate records of all financial transactions.

7. The seventh part of the document discusses the importance of maintaining accurate legal records. It emphasizes that proper legal record-keeping is essential for protecting the organization's interests and ensuring compliance with applicable laws. The text outlines various methods for organizing and storing legal documents, including digital databases and physical filing systems. It also mentions the need for regular reviews and updates to ensure the accuracy of the records.

8. The eighth part of the document discusses the importance of maintaining accurate personnel records. It emphasizes that proper personnel record-keeping is essential for managing the organization's human resources effectively. The text outlines various methods for organizing and storing personnel data, including digital databases and physical filing systems. It also mentions the need for regular updates and reviews to ensure the accuracy of the records.

9. The ninth part of the document discusses the importance of maintaining accurate project records. It emphasizes that proper project record-keeping is essential for tracking progress, managing resources, and ensuring the successful completion of projects. The text outlines various methods for organizing and storing project data, including digital databases and physical filing systems. It also mentions the need for regular updates and reviews to ensure the accuracy of the records.

10. The tenth part of the document discusses the importance of maintaining accurate communication records. It emphasizes that proper communication record-keeping is essential for documenting decisions, tracking progress, and ensuring accountability. The text outlines various methods for organizing and storing communication data, including digital databases and physical filing systems. It also mentions the need for regular updates and reviews to ensure the accuracy of the records.

Q7 2 113-GLAYWIMBROS 17

14 122-113-GLAYWIMBROS 127

RESULT 10

US 10 629-406 42116

1 Sequence 5, Application US/10026-086

2 GENERAL INFORMATION:

3 APPLICANT: NAKAI, Hiroshi

4 APPLICANT: NAKAI, Hiroshi

5 APPLICANT: Bank David K.

6 APPLICANT: Bank David K.

7 TITLE OF INVENTION: EXTRACTING AND ANALYZING TW

8 TITLE OF INVENTION: EXTRACTING AND ANALYZING TW

9 FILE REFERENCE: AD-MICA X 2

10 CURRENT FILING DATE: 2001 12 20

11 PRIOR FILING DATE: 2001 12 20

12 NUMBER OF SEQ. ID NOS: 34208

13 SOFTWARE: Anomax Sequence List and Endline v-ers. 1.1

14 SEQ. ID NO 42116

15 LENGTH: 163

16 TYPE: PR

17 ORGANISM: Homo sapiens

18 FEATURE:

19 OTHER INFORMATION: MAP TO ALLOCATIONS

20 OTHER INFORMATION: EXPRESSED IN LIVER, SKIN, 1.7

21 OTHER INFORMATION: EXPRESSED IN BONE MARROW, 2

22 OTHER INFORMATION: EXPRESSED IN ADIP. TISSUE, 1.5

US 10 629-406 42116

Query Match

Best Local Similarity 44.9% Score 40; Len 7; Length 163

Matches 6; Conservation 4; Mismatches 4; Indels 0; Gaps 0;

Q7 113-GLAYWIMBROS 16

14 122-113-GLAYWIMBROS 145

RESULT 11

US 10 629-406 42116

1 Sequence 5, Application US/10026-086

2 GENERAL INFORMATION:

3 APPLICANT: NAKAI, Hiroshi

4 APPLICANT: NAKAI, Hiroshi

5 APPLICANT: Bank David K.

6 APPLICANT: Bank David K.

7 TITLE OF INVENTION: EXTRACTING AND ANALYZING TW

8 TITLE OF INVENTION: EXTRACTING AND ANALYZING TW

9 FILE REFERENCE: AD-MICA X 2

10 CURRENT FILING DATE: 2001 12 20

11 PRIOR FILING DATE: 2001 12 20

12 NUMBER OF SEQ. ID NOS: 34208

13 SOFTWARE: Anomax Sequence List and Endline v-ers. 1.1

14 SEQ. ID NO 42116

15 LENGTH: 163

16 TYPE: PR

17 ORGANISM: Sphingomonas elodea

US-10-015-127-11090

Query Match

Best Local Similarity 44.9% Score 40; Len 7; Length 163

Matches 6; Conservation 4; Mismatches 4; Indels 0; Gaps 0;

Q7 113-GLAYWIMBROS 16

14 122-113-GLAYWIMBROS 145

RESULT 12

US 10 629-406 42116

1 Sequence 5, Application US/10026-086

2 GENERAL INFORMATION:

3 APPLICANT: NAKAI, Hiroshi

4 APPLICANT: NAKAI, Hiroshi

5 APPLICANT: Bank David K.

6 APPLICANT: Bank David K.

7 TITLE OF INVENTION: EXTRACTING AND ANALYZING TW

8 TITLE OF INVENTION: EXTRACTING AND ANALYZING TW

9 FILE REFERENCE: AD-MICA X 2

10 CURRENT FILING DATE: 2001 12 20

11 PRIOR FILING DATE: 2001 12 20

12 NUMBER OF SEQ. ID NOS: 34208

13 SOFTWARE: Anomax Sequence List and Endline v-ers. 1.1

14 SEQ. ID NO 42116

15 LENGTH: 163

16 TYPE: PR

17 ORGANISM: Sphingomonas elodea

1 Sequence 5, Application US/09647-522

2 GENERAL INFORMATION:

3 APPLICANT: NAKAI, Hiroshi

4 APPLICANT: NAKAI, Hiroshi

5 APPLICANT: Bank David K.

6 APPLICANT: Bank David K.

7 TITLE OF INVENTION: EXTRACTING AND ANALYZING TW

8 TITLE OF INVENTION: EXTRACTING AND ANALYZING TW

9 FILE REFERENCE: AD-MICA X 2

10 CURRENT FILING DATE: 2001 12 20

11 PRIOR FILING DATE: 2001 12 20

12 NUMBER OF SEQ. ID NOS: 34208

13 SOFTWARE: Anomax Sequence List and Endline v-ers. 1.1

14 SEQ. ID NO 42116

15 LENGTH: 163

16 TYPE: PR

17 ORGANISM: Sphingomonas elodea

US 09 647 522 5

Query Match

Best Local Similarity 44.9% Score 40; Len 7; Length 163

Matches 6; Conservation 4; Mismatches 4; Indels 0; Gaps 0;

Q7 113-GLAYWIMBROS 16

14 122-113-GLAYWIMBROS 145

RESULT 13

US 10 015 127 11561

1 Sequence 11561, Application US/10011-127

2 GENERAL INFORMATION:

3 APPLICANT: Bower, Stanley G.

4 APPLICANT: Bower, Stanley G.

5 APPLICANT: Bower, Stanley G.

6 APPLICANT: Bower, Stanley G.

7 TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof

8 TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof

9 FILE REFERENCE: 48 10(15806)B

10 CURRENT FILING DATE: 2001 10 29

11 PRIOR FILING DATE: 2001 10 29

12 NUMBER OF SEQ. ID NOS: 14567

13 SEQ. ID NO 11561

14 LENGTH: 164

15 TYPE: PR

16 ORGANISM: Sphingomonas elodea

US 10 015 127 11561

Query Match

Best Local Similarity 44.4% Score 39.5; Len 7; Length 163

Matches 6; Conservation 1; Mismatches 1; Indels 0; Gaps 0;

Q7 6 GLAYWIMBROS 16

14 104 GLAYWIMBROS 119

RESULT 14

US 10 015 127 11920

1 Sequence 11920, Application US/10011-127

2 GENERAL INFORMATION:

3 APPLICANT: Bower, Stanley G.

4 APPLICANT: Bower, Stanley G.

5 APPLICANT: Bower, Stanley G.

6 APPLICANT: Bower, Stanley G.

7 TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof

8 TITLE OF INVENTION: Sphingomonas elodea genome sequences and uses thereof

9 FILE REFERENCE: 48 10(15806)B

10 CURRENT FILING DATE: 2001 10 29

11 PRIOR FILING DATE: 2001 10 29

12 NUMBER OF SEQ. ID NOS: 14567

13 SEQ. ID NO 11561

14 LENGTH: 164

15 TYPE: PR

16 ORGANISM: Sphingomonas elodea

US 10 015 127 11920

10/1/2002 10:00:00 AM

10/1/2002 10:00:00 AM

0: Gaps 0:

10/1/2002 10:00:00 AM

10/1/2002 10:00:00 AM

10/1/2002 10:00:00 AM

10/1/2002 10:00:00 AM

0: Gaps 0:

10/1/2002 10:00:00 AM

Query Match: 63.5% Score 51.5 DB 2: Length 482,
 Best Local Similarity 70.6% Prod. No. 0.99,
 Matches 42: Conserved 0: Mismatches 2: Indels 1: Gaps 1:

Q7 2 DDDGHLAYIM MGRKSV 17
 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

DE 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 4

S4472
 alkaline serine proteinase 1: Streptomyces sp.

C:Species: Streptomyces sp.

C:Date: 13-Jun-1995 #sequence_revision 13 Jun 1995 #text_change 13 May 2000

C:Accession: S4472

Ref: Yoneda, Y., Ito, T., Ochi, T., Ochi, T.,

submitted to the EMBL Data Library, July 1993

A:Reference number: S4472

A:Accession: S4472

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

Query Match: 57.9% Score 51.5 DB 2: Length 488,

Best Local Similarity 58.8% Prod. No. 0.99,

Matches 42: Conserved 0: Mismatches 2: Indels 1: Gaps 1:

Q7 2 DDDGHLAYIM MGRKSV 17
 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

DE 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 4

A5069

Streptolysin A: Streptomyces protease 1: (27-133,21-3) protease 1: Streptomyces strains

C:Species: Streptomyces strains

C:Date: 07-Jul-1994 #sequence_revision 07 Oct-1994 #text_change 19 May 2000

C:Accession: A5069

Ref: Sudo, S., Kaimori, G., Wakisaka, T.,

1: Biol. Chem. 269, 20167-20171, 1994

A:Title: Streptomyces protease 1: A novel enzyme of the chymotrypsin superfamily

A:Reference number: A5069; M0119412773

A:Accession: A5069

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1457-1510

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1457-1510

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1457-1510

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1457-1510

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1457-1510

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1457-1510

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1457-1510

Ref: Yoneda, Y., Ito, T., Ochi, T., Ochi, T.,

submitted to the EMBL Data Library, July 1993

A:Reference number: S4472

A:Accession: S4472

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1480-1495

A:Cross reference: EMBL:XY117; NBR:170196; FNR:AA52206.1; FID:4196197

C:Superfamily: Streptolysin A

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[illegible]

Query Match 46.1% Score 41: 106 1: Length 196;
Best Local Similarity 46.1% Prod. No. 41;
Matches 4: Mismatches 0: Gaps 0;

97 2 D113LAVIM03R 14
11 11 11 11
10 2 D113LAVIM03R 45

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1: 5A22 HUMAN STANDARD 141: 415 AA
AC P10264
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